











[illegible]

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[illegible][illegible]





beta-6, and probably plays a significant role in mkr beta-3 function. The mkr beta-2 clone was isolated from an embryonic stem cell genomic library. It lacks exon 3, 2 other isoforms, mkr beta-1 (see W08125) and rat mkr beta-4 (see W08127), have also been isolated, and the human exon 5b region (see X24934) has been identified. Based on these sequences, the invention provides methods for identifying agents that block or augment ER beta-6 mediated transcriptional regulation, methods to determine whether ER beta-6 or its isoforms is being expressed in tissues or cells, and methods of identifying and using agents that block the transcriptional regulation of genes by ER beta-6 or its isoforms, which in turn mediates other biological and pathological processes. Gene therapy expression of ER beta-6 is envisaged.

XX  
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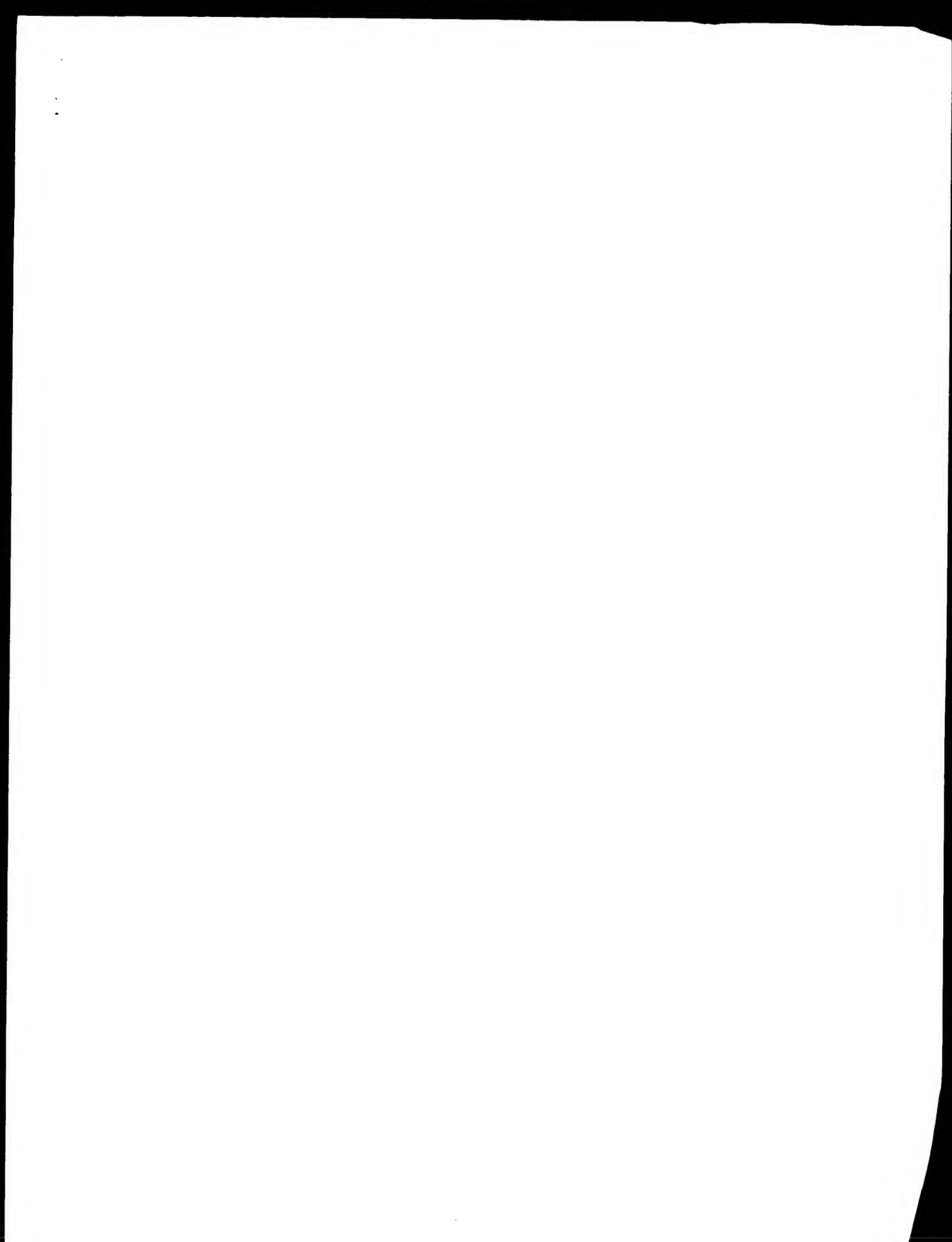
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Best Local Similarity: 81.4%; Prod. No. 8, Jan-206;  
Matches: 441; Conservative: 25; Mismatches: 35; Indels: 39; Gaps: 1;

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TISSUE: ovary;  
 MEDLINE: 98348189; PubMed: 9685228;  
 RA In R., Leysen R., Dotzlaw H., Murphy L.J., Murphy L.C., Watson P.H.;  
 "Estrogen receptor-beta mRNA variants in human and murine tissues";  
 Mol. Cell. Endocrinol. 138:199-203(1998).  
 [17]  
 RP SEQUENCE OF 1-69 FROM N.A.  
 RA L.L.C., Ishida K.;  
 "Cloning and characterization of the estrogen receptor beta gene  
 promoter";  
 Biochim. Biophys. Acta 1140:1-10(1994) to the PubMed/Genbank/EMBL databases  
 [18]  
 RP CHARACTERIZATION.  
 RA MEDLINE: 97467383; PubMed: 9325333;  
 RA Page P., Taylor J., Sutherland-Graham S., Coombes R.C., Ali S.,  
 "Human estrogen receptor beta binds DNA in a manner similar to and  
 dimerizes with estrogen receptor alpha";  
 J. Biol. Chem. 272:25832-25838(1997)  
 [19]  
 RA FURTHER, BINDS ESTROGEN WITH AN AFFINITY SIMILAR TO THAT OF ER-  
 ALPHA, AND ACTIVATES EXPRESSION OF PEROXYPHASE GENES CONTAINING  
 ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.  
 ISOPFORM BETA-CX LACKS LIGAND BINDING ABILITY AND HAS NO OR ONLY  
 VERY LOW ERE BINDING ACTIVITY RESULTING IN THE LOSS OF LIGAND-  
 DEPENDENT TRANSCRIPTIONAL ACTIVITY. DNA-BINDING BY ER-ALPHA AND  
 BETA IS RAPIDLY LOST AT 37 DEGREES CELSIUS IN THE ABSENCE OF  
 LIGAND WHILE IN THE PRESENCE OF 17 BETA-ESTRADIOL AND 4-HYDROXY-  
 TAMOXIFEN LOSS IN DNA-BINDING AT ELEVATED TEMPERATURE IS MORE  
 GRADUAL.  
 [20]  
 RA SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-  
 ALPHA. ISOPFORM BETA-2/CX PREFERENTIALLY FORMS A HETERODIMER WITH  
 ER-ALPHA PREFER THAN ER-BETA AND INITIATES DNA-BINDING BY ER-ALPHA.  
 [21]  
 RA SUBCELLULAR LOCATION: NUCLEUS.  
 [22]  
 RA ALTERNATIVE PRODUCTS: 8 ISOPFORMS: BETA-1 (SHOWN HERE), BETA-2/CX,  
 BETA-2A, BETA-3, BETA-4, BETA-5, BETA-5A AND BETA-6; ARE PROVIDED  
 BY ALTERNATIVE SPLICING.  
 [23]  
 RA TISSUE SPECIFICITY: ISOPFORM BETA-1 IS EXPRESSED IN TESTIS AND  
 OVARY, AND AT A LOWER LEVEL IN HEART, BRAIN, PLACENTA, LIVER,  
 SKETAL MUSCLE, STOMACH, THYMUS, PROSTATE, COLON, BONE MARROW,  
 MAMMARY GLAND AND UTERUS. ALSO FOUND IN COLON AND LIVER TUMORS.  
 [24]  
 RA OVARIAN TUMOR CELL LINES, BUT NOT IN COLON AND LIVER TUMORS.  
 [25]  
 RA ISOPFORM BETA-2 IS EXPRESSED IN SPLEEN, THYMUS, TESTIS AND OVARY  
 AND AT A LOWER LEVEL IN SKETAL MUSCLE, PROSTATE, COLON, SMALL  
 INTESTINE, LEUKOCYTES, BONE MARROW, MAMMARY GLAND AND UTERUS.  
 [26]  
 RA ISOPFORM BETA-3 IS FOUND IN TESTIS. ISOPFORM BETA-4 IS EXPRESSED IN  
 TESTIS, AND AT A LOWER LEVEL IN SPLEEN, THYMUS, OVARY, MAMMARY  
 GLAND AND UTERUS. ISOPFORM BETA-5 IS EXPRESSED IN TESTIS, PLACENTA,  
 SKETAL MUSCLE, SPLEEN AND LEUKOCYTES, AND AT A LOWER LEVEL IN  
 HEART, LUNG, LIVER, KIDNEY, PANCREAS, THYMUS, PROSTATE, COLON,  
 SMALL INTESTINE, BONE MARROW, MAMMARY GLAND AND UTERUS. NOT  
 EXPRESSED IN BRAIN.  
 [27]  
 RA A LIGAND-BINDING DOMAIN AND A C-TERMINAL, STEROID-BINDING DOMAIN  
 [28]  
 RA 1-1: DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,  
 A LIGAND-BINDING DOMAIN AND A C-TERMINAL, STEROID-BINDING DOMAIN  
 [29]  
 RA 1-1: SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.  
 [30]  
 RA 1-1: SUBFAMILY:  
 [31]  
 RA THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL Outstation  
 at the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))

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 DR InterPro: IPR001728;  
 DR Pfam: PF00104; hormone\_rec\_1;  
 DR Pfam: PF00105; zf-C4; 1;  
 DR PRINTS: PR0047; SIKOUPINGER;  
 DR PRINTS: PR00350; VITAMINDK;  
 DR PRINTS: PR00448; STROPHOMER;  
 DR PRINTS: PS00546; THYROIDHORM;  
 DR PROSITE: PS00031; NUCLEAR\_RECEPTOR; 1;  
 DR Receptor: Transcription regulation; DNA-binding; Nuclear protein;  
 KW Zinc-finger; Steroid-binding; Alternative splicing; Phosphorylation.  
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 FT 1001

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DR	InterPro: IPRO003124; -						
DE	InterPro: IPRO006486; -						
DR	InterPro: IPRO01628; -						
DR	InterPro: IPRO01723; -						
DR	InterPro: IPRO01728; -						
DR	Pfam: PF001104; hormone_rec_1.						
DE	Pfam: PF001105; zt-c4_1.						
DE	PRINTS: PR00647; STREPTINDER.						
DE	PRINTS: PR00350; VITAMINDR.						
DE	PRINTS: PR00398; STERHOXONER.						
DE	PRINTS: PR00546; THYROIDHORM.						
DR	PROSITE: PS00671; NUCLEAR_RECEPTOR; 1.						
KW	Receptor; Transcription regulation; DNA-binding; Nuclear protein;						
RZ	Zinc finger, steroid binding; Phosphorylation.						
FT	DOMAIN 1 145 MODULANT.						
FT	DNA_BIND 146 211 NUCLEAR RECEPTOR-TYPE.						
FT	ZN_FING 146 166 C4-TYPE.						
FT	ZN_FING 182 206 C4-TYPE.						
FT	DOMAIN 212 527 STEROID-BINDING.						
FT	MOL_RES 84 84 PHOSPHORYLATION (BY SIMILARITY).						
FT	MOL_RES 485 485 PHOSPHORYLATI-ON (BY SIMILARITY).						
FT	CONFLICT 60 60 N -> D (IN REF. 2).						
SO	SEQUENCE 527 AA; 59031 MW; 9CFEFD6F4FCB84 CRC64;						
<hr/>							
Query Match	87.8%;	Score 2463.5;	Hl 1;	Length 527;			
Best Local Similarity	87.9%;	Prod. No. 4,56-189;					
Matches 466;	Conservative 22;	Mismatches 39;	Indels 4;	Gaps 1;			
<hr/>							
OY	1 MDYNSTSLNSVSSVNCSCSLPLEHCSTYTHSSVYSIHIEYDAMPYSPYAWNVSYPS 60						
DB	1 MDVNNSSLSLNISVSVNCGSSLPLPDLPGYLVSPSVVASRHFYSAYVFYSAVVNNSTPN 60						
OY	61 NVNI MEGAPGQII SPNWLP LPIALSG VHQGLSH YACAGASGFLA SLEHLIV 120						
DB	61 --NSEGDPRQRTTSNPVLMP PGHSIPALMGQPSVLYAEHQKSMPEIKSLRHLPVN 117						
OY	121 RETLKRRVSNPCASVYVQSKLHPAVCSDFASCYHYGVMSCECAAFKRSLTGH 180						
DB	118 RETLKRAASGSASATLSSTRSRKAARFAVCADLASRIHGVMSLTADNATIRKSLTGH 177						
OY	181 NDYLCVATNQETDENPKSSQA TLRKYCYGVGMVNTSEFHQNYSLVNRGTAAQLH 240						
DB	178 NRYLFVATNQELLENPFSLQNGC PTEVMYVYTFEFQYTVVDSQRHPCQLH 237						
OY	241 CGAGAKSGCGAPVPVPELLDALSPQIVTLLEAPRHVILSRSPAPFPASMMSLTK 300						
DB	238 CLSKTRKGSGMTRVKELLASLSPQIVTLLEAPRHVILSRSTPTTASMMSLTK 297						
OY	301 LADELVIHMI SWAKRIGCVLESIPGQVIMTESQMVLMQMLMPSLDHPGKLIFAPDL 366						
DB	298 LADELVIHMI SWAKRIGCVLESIPGQVIMTESQMVLMQMLMPSLDHPGKLIFAPDL 357						
OY	361 VLAKKEGVGGLLETFEMALTATSPFER KLRHFYICVAAML IRESMYV VTAQAQL 420						
DB	358 TLIDRPCKVEGLILEFDMLATTSPTRELKIQKHQYLVANMILLNSRPSATAQQLA 417						
OY	421 LEESELALILNAVITALVWY FAFSTVS LGSGES GNLMT LSHVDNDZROMHLIRF 480						
DB	418 EGGHLLHLIAVTDAVWY FAFSGES LGSGESQ ANML SHVDNDZROMHLLIRF 477						
OY	481 CKRVVYVDLLEMLNAVILPOTKSLTGSEVSTATFSSESLSANGSQ 540						
DE	478 CKRVVYVDLLEMLNAVILPOTKSLVTSPELVSESPTSFKPDQG 527						
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RESULT 6							
ID ESRL_SHEEP	STANDARD;	PKT;	527 AA.				
AC Q9TUI5; Q9TUT6;							
DT 01-oct-2000 (Ref. 40, Created)							
DT 01-oct-2000 (Ref. 40, Last sequence update)							
DT 01-oct-2000 (Ref. 40, Last annotation update)							

DE ESTROGEN RECEPTOR BETA (ER-BETA).  
 EN ESR2 OR NR3A2.  
 OS ERKARFODI; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OT Mammalia; Eutheria; Cerealia; Eutheria; Primates; Hominidae;  
 OX Homo; Caprinae; Ovis.  
 PN 111.  
 RP SEQUENCE FROM N.A. (15-1688; BETA AND BETA 1).  
 RS 11500; ovary.  
 RA Anderson H.; Blusky R M.; Papp W F.; Nephew K P.;  
 RI Cloning and expression of estrogen receptor beta in the ovine  
 ovary.  
 RL Submitted (AUG-1999) to the EMBL/Genbank/Tran databases.  
 RC 1. FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF  
 ER-ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING  
 ESTROGEN RESPONSE ELEMENTS (PRE) IN AN ESTROGEN-DEPENDENT MANNER.  
 CC 1. SUBUNIT: BINDS DNA AS A HOMODIMER, CAN FORM A HETERODIMER WITH ER-  
 CC 2. ALFA (BY SIMILARITY).  
 CC 3. SUBCELLULAR LOCATION: NUCLEAR.  
 CC 4. ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS: BETA (SHOWN HERE) AND  
 CC 5. BETA-1. ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC 6. BETA-1 IS COMPOSED OF EFFECT-1-MANIN, A MODULATING N-TERMINAL DOMAIN,  
 CC 7. A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.  
 CC 8. SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.  
 CC 9. NRS SUBFAMILY.  
 CC 10. THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC 15. entities requires a license agreement (see http://www.ebi.ac.uk/ebd/ on the  
 CC 16. or send an email to license@ebi.ac.uk).  
 CC 17. EMBL: AF177946; A055772.1;  
 CC 18. EMBL: AF267109; AAF1745.1;  
 CC 19. HSSB: F04472; Hbcp.  
 CC 20. InterPro: IPR00424;  
 CC 21. InterPro: IPR00546;  
 CC 22. InterPro: IPR01628;  
 CC 23. InterPro: IPR01724;  
 CC 24. Pfam: PF0134; hormone\_f001.1;  
 CC 25. Pfam: PF0135; Z1-01.1;  
 CC 26. PRINTS: PR00437; SIBRODIMER.  
 CC 27. PRINTS: PR00450; VITAMINR.  
 CC 28. PRINTS: PR00498; SIBRODIMER.  
 CC 29. PROSITE: PS00631; NUCLEAR RECEPTOR 1;  
 CC 30. PROSITE: PS00632; TRANSCRIPTION REGULATOR DNA-BINDING; Nuclear protein;  
 CC 31. PROSITE: PS00633; STEROID-BINDING; Allosteric splicing; Phosphorylation.  
 CC 32. DOMAIN: 1 145 MODULATING.  
 CC 33. ERKARFODI 146 211 NUCLEAR RECEPTOR TYPE.  
 CC 34. ERKARFODI 146 166 64-TYPE.  
 CC 35. ERKARFODI 146 206 64-TYPE.  
 CC 36. ERKARFODI 146 212 64-TYPE.  
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 CC 98. ERKARFODI 146 212 64-TYPE.  
 CC 99. ERKARFODI 146 212 64-TYPE.  
 CC 100. ERKARFODI 146 212 64-TYPE.

DB 61 ---- NSR62;PROT;ESTROGEN RECEPTOR BETA (ER-BETA).  
 CC 121 ERKARFODI; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC 122 Mammalia; Eutheria; Cerealia; Eutheria; Primates; Hominidae;  
 CC 123 Homo; Caprinae; Ovis.  
 CC 124 111.  
 CC 125 SEQUENCE FROM N.A. (15-1688; BETA AND BETA 1).  
 CC 126 RS 11500; ovary.  
 CC 127 RA Anderson H.; Blusky R M.; Papp W F.; Nephew K P.;  
 CC 128 Cloning and expression of estrogen receptor beta in the ovine  
 CC 129 ovary.  
 CC 130 Submitted (AUG-1999) to the EMBL/Genbank/Tran databases.  
 CC 131 FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF  
 CC 132 ER-ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING  
 CC 133 ESTROGEN RESPONSE ELEMENTS (PRE) IN AN ESTROGEN-DEPENDENT MANNER.  
 CC 134 SUBUNIT: BINDS DNA AS A HOMODIMER, CAN FORM A HETERODIMER WITH ER-  
 CC 135 ALFA (BY SIMILARITY).  
 CC 136 SUBCELLULAR LOCATION: NUCLEAR.  
 CC 137 ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS: BETA (SHOWN HERE) AND  
 CC 138 BETA-1. ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC 139 BETA-1 IS COMPOSED OF EFFECT-1-MANIN, A MODULATING N-TERMINAL DOMAIN,  
 CC 140 A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.  
 CC 141 SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.  
 CC 142 NRS SUBFAMILY.  
 CC 143 THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC 144 between the Swiss Institute of Bioinformatics and the EMBL outstation  
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 CC 146 use by non-profit institutions as long as its content is in no way  
 CC 147 modified and this statement is not removed, usage by and for commercial  
 CC 148 entities requires a license agreement (see http://www.ebi.ac.uk/ebd/ on the  
 CC 149 or send an email to license@ebi.ac.uk).  
 CC 150 EMBL: AF177946; A055772.1;  
 CC 151 EMBL: AF267109; AAF1745.1;  
 CC 152 HSSB: F04472; Hbcp.  
 CC 153 InterPro: IPR00424;  
 CC 154 InterPro: IPR00546;  
 CC 155 InterPro: IPR01628;  
 CC 156 InterPro: IPR01724;  
 CC 157 Pfam: PF0134; hormone\_f001.1;  
 CC 158 Pfam: PF0135; Z1-01.1;  
 CC 159 PRINTS: PR00437; SIBRODIMER.  
 CC 160 PRINTS: PR00450; VITAMINR.  
 CC 161 PRINTS: PR00498; SIBRODIMER.  
 CC 162 PROSITE: PS00631; NUCLEAR RECEPTOR 1;  
 CC 163 PROSITE: PS00632; TRANSCRIPTION REGULATOR DNA-BINDING; Nuclear protein;  
 CC 164 PROSITE: PS00633; STEROID-BINDING; Allosteric splicing; Phosphorylation.  
 CC 165 DOMAIN: 1 145 MODULATING.  
 CC 166 ERKARFODI 146 211 NUCLEAR RECEPTOR TYPE.  
 CC 167 ERKARFODI 146 166 64-TYPE.  
 CC 168 ERKARFODI 146 206 64-TYPE.  
 CC 169 ERKARFODI 146 212 64-TYPE.  
 CC 170 ERKARFODI 146 212 64-TYPE.  
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 CC 198 ERKARFODI 146 212 64-TYPE.  
 CC 199 ERKARFODI 146 212 64-TYPE.  
 CC 200 ERKARFODI 146 212 64-TYPE.





CC	ESTROGEN RECEPTOR HETEROLOGOUS (ERR) IN AN ESTROGEN-DEPENDENT MANNER
CC	SUBUNIT FORMED FOR A HORMONE-RECEPTOR CAN FORM A HETERODIMER WITH PR-
CC	ALPHA.
CC	-1 SUBCELLULAR LOCATION: NUCLEAR.
CC	-1 TISSUE SPECIFICITY: LIVER.
CC	-1 INDUCTION: BY 17-BETA-ESTRADIOL.
CC	-1 DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC	A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC	-1 SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC	M33 SUBFAMILY.
CC	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed, usage by and for commercial
CC	entities requires a license agreement (See <a href="http://www.ebi.ac.uk/submit/">http://www.ebi.ac.uk/submit/</a>
CC	or send an email to <a href="mailto:license@isb.sib.ch">license@isb.sib.ch</a> ).
CC	
DR	EMBL: AH003456; BAAI9851.1;
DR	BSSP: P03472; HGP.
DR	InterPro: IPR000536;
DR	InterPro: IPR001628;
DR	InterPro: IPR001723;
DR	Pfam: PF00104; hormone_rec_1.
DR	Pfam: pf00105; zf-C4_1.
DR	PRINTS: PR00047; SteroidRecep
DR	PRINTS: PR00106; SteroidRecep
DR	PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
FW	Description: Transcription regulation. DNA-binding: Nuclear protein;
KM	Zinc-finger; Steroid-binding.
FM	DOMAIN 15 170 MODULATING
FT	DNA_BIND 171 34 PROTEIN_PPTYPE
FT	ZN_FING 171 191 C4-TYPE
FT	ZN_FING 207 281 C4-TYPE
FT	DOMAIN 277 573 STEROID-BINDING
SC	SEQUENCE: 573 AA; 63420 MW; 6254C1D9B9A9DC CYP64;
CC	
CC	Query Match 55.2%; Score 1549; DB 1; Length 573;
CC	Best Local Similarity 57.7%; Pred. No. 4; Le-116;
CC	Matches 113; Colocalized 62; Mismatches 121; Indels 46; Gaps 10.
CC	
CC	1 PSYMNQSSTIPSPNITIPSPSYSHSYSHSEVYAMTYSEFAVMYSITPSVTILEGCR-- 69
DB	33 PLTMNGALPALMSHSAVCPSPETPDSSIDYALITTSPEILLH-----GGPAVP 82
CC	70 -----SGEATSPNVWQ---PPN SPVYNKQI SHLYAFQRKSPWCRAKSLEHTLVNRK 122
DB	83 ESFAAQOSTLSPSLFWAHGNCHNCVSPLADFDQPIPLYREPANSMARKPLEH----GO 137
CC	123 ELKKKSNINCASPVGRPS-----KRARECAVCSYASGYNHGWMSCECKAKFFR 175
DB	138 AQTSKIAGKMAESERGISISVGCFACKGMHCMDACVCHOYASGYIHGWMSCDECKAPFR 197
CC	176 ELTDHNAYCTA-N-Q-T-LTPSPSYLAHTRKYTVYAMKTCSPFPCTPGCYIVENQRA 245
DB	198 SLGHNGICGFATRCGLTEKNRKSGCDRLPYGEVCMKCGVPEFCYTPGARHPMP 257
CC	236 D--EQDICAGKA---KRSQHARVRVELLDALSPEEDVLTLAEPRHY-LISRTSAP 285
DB	258 HELIELAQDTQAATQAPRGVAVDQTQFAOSSATTPQLNRITFEPRPETYLMEKEKKRP 317
CC	290 TPFSMMSTLERLKRELVEHNSIAKKIRPGEVLSIPGVNLTSCSWEVNIMMLTMRSTD 349
DB	318 THDSMMSTLNIAKLKVLMISMARRKIPGVVELDSIQVHLKSCWEVLEMLDMRRSD 377
CC	450 HKSKLPAPRLVDIGRQCKVVEGLEELFLMDLATTSFPRRLKHQKEYLCVKAMILNSS 409
DB	478 HKPKLIVPRDLKINRDESGVEGLEELFLMDLATSFPRRLKIKREBYVCALKAILNP 437
CC	410 MYPLVATL-GIADSRKLAHLINVAVALAWVAKNSTSSQSQMRLANLMLSHVBA 468

Db	438	LCITSSSENEFELESNKLLIMHJDSVTIAI WFT AKKALIFPOOOSARHAIIMLLIAHIRH	497
QY	469	SNKSMCHLNMKRNKVEEYVYLLEHIAVLRDCKKQK LGGKQKDAVSKSTSTSTST	528
Db	498	SNKSMCHLNMKRNKVEEYVYLLEHIAVLRDCKKQK LGGKQKDAVSKSTSTSTST	550
QY	529	SNKSMCHLNMKRNKVEEYVYLLEHIAVLRDCKKQK LGGKQKDAVSKSTSTSTST	560
Db	551	SNKSMCHLNMKRNKVEEYVYLLEHIAVLRDCKKQK LGGKQKDAVSKSTSTSTST	582

## RESULT 11

1D KRB1

01-00  
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COX	NCBI
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Fri Apr 20 09:00:54 2001

us-08-906-365-2.rsp

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Page 14

OpenPro version 4.5  
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OpenPro search, using SW model

Run date: April 18, 2001, 10:13:51 / Search time 4398.37 Seconds

(without alignments) 5265.456 Million cell updates/sec

Hit list: US08-906-365-1

Search score: 1.686

Search time: 1.0

Search score: 1.686

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Search score: 1.686

Search time: 1.0

Search score: 1.686

Search time: 1.0

Search score: 1.686

Search time: 1.0

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Search time: 1.0

Search score: 1.686

Search time: 1.0

Search score: 1.686

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83: em\_h081:  
84: em\_h082:  
85: em\_h083:

Prod. No. is the number of results produced by chosen parameters  
score greater than or equal to the score of the result found printed  
and is derived by analysis of the total score distribution.

# SUMMARY

Result No.	Score	Query Match	Length	Hit	Accession
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3	1684.4	99.8	1898	61	AF11427
4	1684.4	99.8	1647	48	AX02440
5	1496.4	89.8	2041	110	AF011429
6	1496.4	89.8	2745	10	AF011429
7	1496.4	89.7	1594	8	AF011429
8	1485.6	88.1	1651	48	AF011429
9	1485.6	88.1	1460	48	AX02440
10	1485.6	88.1	1460	61	AF11427
11	1485.6	88.1	1460	61	AF11427
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Db 867 CTGCTGTCAGCGATTACGATCCGATATCACTATGAGAGCTGTGTTCTGTGAAAGATGTA 926
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Db 2007 ACTGA 2011

RESULT 3
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DEFINITION Sequence 24 from patent EP0798378.
ACCESSION A65127
VERSION A65127.1 GI 4530491
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1898)
AUTHORS Mosselman, S. and Dijkema, R.
TITLE Estrogen receptor
JOURNAL Patent, EP 0798378-A, 01-02-1997;
AKZO NOBEL NV (NL)
COMMENT other publication: CA 220423, 19970926,
FEATURES location/Qualifiers
SOURCE 1..1898
BASE COUNT 452 a 506 c 501 g 439 t
ORIGIN

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Best Local Similarity 99.9% Pred. No. 0;
Matches 1668; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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[illegible]

DEFINITION	Homo sapiens estrogen receptor beta2 splice variant mRNA, complete cds.
ACCESSION	AF051428
VERSION	AF051428.1
KEYWORDS	61..961558
SOURCE	.
ORGANISM	human.
REFERENCE	Homo sapiens Lutaretz, M., Kasper, C., Gherghel, A., Velez, L., Ballesteros, J., Mammala, E., Bhatia, P., Primateas, F., Cataphino, H., Homidaghi, H., Moore, J.T., McKee, D.D., Moore, L.B., Jones, S.A., Su, J.-T., Horne, R.L., Klee, S., Klee, S., Klee, S., Klee, S., Klee, S., Klee, S., Cloning, ligand binding and functional activity of human Estrogen Receptor beta isoforms
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 2041)
AUTHORS	Moore, J.T., McKee, D.D., Moore, L.B., Jones, S.A., Su, J.-T., Horne, R.L., Klee, S., Klee, S., Klee, S., Klee, S., Klee, S., Klee, S., Direct Submission
TITLE	Submitted (25 FEB 1998) Molecular cloning, ligand binding, and functional activity of human Estrogen Receptor beta isoforms
JOURNAL	Drive, RTP, NC 27709, USA
FEATURES	Location/Qualifiers
source	1..2041
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Df	387 GCAAGCTGTTTTCTCAGCGTGATCTGCAGGAATGATGATATAAAAATCACCATCTACGC 446
OY	122 taattctccttctcctaacaactcagatcaatcgaatctaaccttgagacagatcca 181
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OY	302 gtccgagaccacaaagcccaatgagtgttgttggtaacagcttgagagcttctctctt 361
Df	627 GTCCGATACACCAAGAAGGTAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 686
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DEFINITION Homo sapiens mRNA for estrogen receptor beta cX, complete cds.
ACCESSION AB006589
VERSION AB006589.1 GI:3345671
KEYWORDS estrogen receptor beta cX.
SOURCE Homo sapiens cDNA clone.
ORGANISM Homo sapiens
Eukaryota; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 3593)
Ogawa,S.
REFERENCE Direct Submission
AUTHORS Submitted (13-APR-1997) to the EMBL/GenBank/CCDS databases. Sumito
TITLE (Ogawa, Sallama Medical School), Department of 2nd Biochemistry; 38
TADPNA: Morioka, Miyazaki, Iruma-shi, Saitama 350-0495, Japan
(M-mail: shogawa@sallama-med.ac.jp, Tel:81-492-76-1490,
Fax:81-492-94-9751)
2 (sites)
Ogawa,S., Inoue,S., Matsuda,T., Tanaka,A., Hosoki,T., Ouchi,Y., and
Miyazaki,M.
JOURNAL Molecular cloning and characterization of human estrogen receptor
MEDLINE beta cX: A potent inhibitor of estrogen action in human
FEATURES
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     /translation="MTRRGLCOLRGLRGRNRSGLRRLRHSRYTSSVSHHRTT
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     YGVSCEKRAEFEPSTLQINLVTPVNPVNTLQNNKRSQVRLPKRYVTVVKNV
     SRRRGGYLVLPGRSALDEGLRAGKAKRSQSHAPVPLILMLSPQVLTLLLEAE
     ERLHLSLAFELHLSHMRSLPLAEGLVHMLQWAFIQLVEETSLPVEVLT
     LMYVLTMLQMLRPSLTLPRLTLPVWLVLPGRVLTLPRLMLATLSPELPLI
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1363  atatacaactctctctctatatacagctcagctatctcagctatctcagctatctat 1422
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Oy	1303	1460	145.3	5e-32	1453	1453	7	0
Db	1261	1460	145.3	5e-32	1453	1453	7	0
Oy	1363	1460	145.3	5e-32	1453	1453	7	0
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Oy	1423	1460	145.3	5e-32	1453	1453	7	0
Db	1381	1460	145.3	5e-32	1453	1453	7	0
Oy	1483	1460	145.3	5e-32	1453	1453	7	0
Db	1441	1460	145.3	5e-32	1453	1453	7	0
Oy	1543	1460	145.3	5e-32	1453	1453	7	0
Db	1501	1460	145.3	5e-32	1453	1453	7	0
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Fri Apr 20 09:00:44 2001

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Page 18













[illegible]

RESULT	6
T88412	
ID	T88412 Standard: cDNA; 144 bp.
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AC	T88412:
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DE	Human estrogen receptor protein cDNA.
XX	
KW	estrogen receptor protein; steroid; alternative splicing; estradiol;
FM	estrogen; estradiol; screening; ds.
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OS	Homo sapiens.
XX	
PN	EP798378-AZ.
XX	
PD	01-OCT-1997.
XX	
PF	25-MAR-1997; 97EP-020090A.
XX	
PK	22-NOV-1996; 96EP-020284
XX	
PR	26-MAR-1995; 96EP-020062D.
XX	
PA	(AKO ) AKZO NOBEL NV.
XX	
P1	Dj Kema R, Mosseman S;
XX	
PI	WP1: 1997-47182/44.
XX	
DR	P FSDB: W44212.
XX	
PT	DNA encoding estrogen receptor - useful in screening assay to
XX	identify novel ligands or hormonal analogues
XX	
PS	Claim 5; Page 13-14; 4Fig; English.
XX	
CC	This sequence encodes a novel estrogen binding protein. The cDNA
XX	sequence which encodes this protein can be identified by a probe
CC	resulting in the detection of additional transcripts (see T88412).
CC	This receptor is able to bind and be activated by estradiol, estrone and by
CC	estrone, it can be used in a screening assay for the identification of new
CC	drugs e.g. novel ligands or hormonal analogues.
XX	
SO	Sequence 1444 bp; 347 A; 478 C; 406 G; 908 T; 9 others.





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NW estrogen-response element, ovary, prostatic osteoporosis; ds.
OS Bos taurus.
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XX FT /product= "ER-beta"
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XX PD 09-MAR-2000.
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XX PF 27-AUG-1998; 98DE-1039115.
XX
XX PR 27-AUG-1998; 98DE-1039115.
XX
XX (IHVH-) THE INST HORMON & FORTIFIAN/JUNOS.
XX
XX Walther N.
XX
XX WP1: 257690/23.
XX
XX DR P-PSDB: Y51946.
XX
XX
XX New bovine estrogen-beta receptor, useful for identifying specific
XX ligands, potentially used for treating cancer and osteoporosis
XX
XX Claim 4: Page 6-8; 20pp; German.
XX
XX
XX This invention describes a novel isolated bovine estrogen receptor-beta
XX (ERB) which has anticancer and anti osteoporosis activity. ERB is a
XX transcriptional transactivator that activates estrogen-dependent
XX transcription of genes that include an estrogen-response element. It is
XX significantly less active than estrogen receptor-alpha. ERB (also, its
XX isoforms and peptides containing its ligand-binding domain), nucleic acid
XX (111) encoding them, or vectors or constructs of ERB, particularly specific
XX ligands that do not bind to the estrogen receptor-alpha. These ligands
XX are potentially useful for treating ERB-associated disorders,
XX particularly cancer of the ovary or prostate, or osteoporosis. This
XX sequence encodes the bovine ER-beta protein described in the method of
XX the invention.
XX
XX Sequence 1820 BP; 446 A; 491 C; 478 G; 405 T; 0 other.
XX
XX
XX Query Match 73.6%; Score 1241.2; EB 21; Length 1820;
XX Best Local Similarity 86.9%; Pred. No. 0;
XX Matches 1979; Conservative 0; Mismatches 198; Indels 4; Gaps 1;
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XX DB 1 taaaaactcaacatctaaccttaactctctctctctctctctctctctctctct 60
XX 1111111111111111111111111111111111111111111111111111111
XX QY 161 taaaactcaacatctaaccttaactctctctctctctctctctctctctctct 220
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RESULT 9  
 ID 28537  
 XX 28537 standard; cDNA: 1820 BP.  
 AC 28537  
 XX 28537  
 DT 23-JUN-2000 (first entry)  
 XX  
 DE Bovine ER-beta cDNA.  
 KW Homo sapiens: estrogen receptor beta; anti-cancer anti-osteoporosis;  
 KW transcriptional transactivator; estrogen dependent transcription; cancer.

[illegible][illegible]







1b	1866	gcacagcagccatcttgacacgacgttacacatgcccgaggctggatgattcgatttcgaagaagtgg	1445
1c	1429	cacttctttctcccaaaagcaccatcttgccttggacaacctcccaaacctctcccacact	1487
1d	1446	aactcctctcccaaaaacgtaactctgctctgggccaacccctcgaatgctctcttcacatgt	1505
1e	1468	cagatcatctaatctaacagagagctctctgaacatactcgtccacatctgaagtcgaaaaaatgtagt	1547
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1k	1668	ccccatctctatcatctgcttatgatgctctcgaatgcctccacatgctctccagatgcacgtc	
1l	1686	ccccatctctatcatctgcttatgatgctctcgaatgcctccacatgctctccagatgcacgtc	
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XX	RESULT 1A		
XX	XZ49v5f Standard; cDNA: 1704 bp.		
XX	XZ49v35f		
XX	Z1-30N-1994 (first entry)		
XX	Muscle cAMP-dependent protein kinase receptor beta clone mEPbeta-3.		
XX	mESTOAPB RECEPTOR; ER beta-v3; ER beta-G2 mouse; tumour; diagnosis;		
XX	library; ds.		
XX	Mus musculus.		
XX	Key:	Accession/containers	
FH	xxxxx	U49_1205	
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XX		/number=58	
FN	W09965[70] A1.		
XX	04-FEB-1999.		
XX	Z8-JUL-1998:	98WD-U515539.	
XX			
XX	xx J01-1997:	97DS-u054210.	
XX	Z8-JUL-1997:	97DS-u053859.	
XX	(UYVA ) UNIV YALE.		
XX	Denton R., Franson C., Gallien R., Rischo-Rigon M.		
XX	WEI: 1999 14285/212.		
XX	J-PSDB: W09128.		
XX	Human osteonin receptor beta-3 - useful in treating and monitoring		
XX	tumours		
XX	Examined by EIC (LJ WFF) Endlich.		
XX	The present sequence is the coding region of the murine complete		
XX	ostonin receptor beta (ER beta-C) cDNA clone mER beta-3, which		
XX	encodes a 67 amino acid protein (see W98128). The gene contains		
XX	7 exons, including the newly described exon 5B, which is not found		
XX	in ER beta-1. Exon 5B is located in the ligand binding domain of		
XX	mER beta-4, and probably plays a significant role in mER beta-3		
XX	function. The mER beta-3 clone was twice isolated using 2-		
XX	spharato procedures: RT-PCR of mRNA; and amplification from a		
XX	mouse embryonic stem cell derived DNA library. 2 Alternatively,		

[illegible]

















[illegible]

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1 Sequence 3, Application US/08481970
2 Patent No. 5859310
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RESULT 8
US-08-693-940-2
Sequence 2, Application US/08693940
Patent No. 633027
GENERAL INFORMATION:
APPLICANT: Yee, Jinn-Kuan
APPLICANT: Fiedman, Theodore
APPLICANT: Chen, Shin-Tai
TITLE OF INVENTION: Inducible Expression System
TITLE OF INVENTION: Useful in the Generation of Packaging Cell Lines for
TITLE OF INVENTION: Pseudotyped Retroviral Vectors
NUMBER OF SHOTS/FILES: 3
CORRESPONDENCE ADDRESS:
ADDRESS: Bozicevic & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASTSHO for Windows Version 2.0

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: us/08/693,940
FILING DATE: 07 Apr 1996
CLASSIFICATION: A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Francis, Carol L.
REGISTRATION NUMBER: 36,513
REFERENCE/EXCERPT NUMBER: 6510-055001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
TELEFAX: 650-327-3231
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1956 base pairs
TYPE: nucleic acid
STANDARDNESS: single
TOPOL/KEY: Linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..1953
OTHER INFORMATION:
US-08-693-940-2

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Query Match 16.0%; Score 285.6; DB 3; Length 1956;
Host Local Similarity 63.8%; Prod. No. 1,30-68;
Matches 467; Conservative 0; Mismatches 259; Indels 6; Gaps 2;

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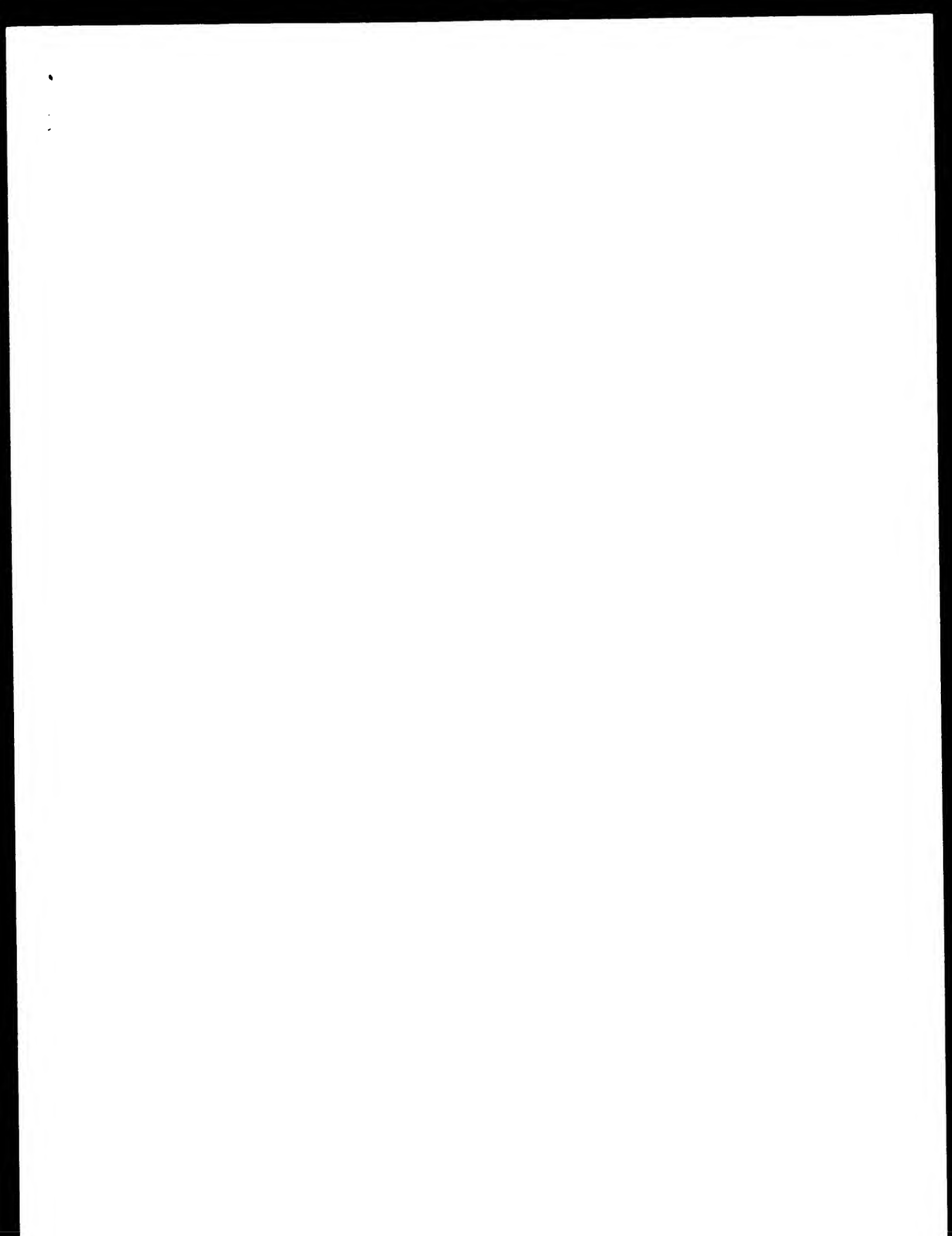


Fri Apr 20 09:00:46 2001

us-08-906-365-1.rni

Page 13

Search completed: Apr 19, 2001, 05:16:20  
Index time: 41576 sec



GeneCore version 4.5  
Copyright (c) 1994 - 2000 CompuGen Ltd.

GM nucleotide > nucleotide search, using SW model

Run on: April 18, 2001, 09:44:24 : Search time 2082.96 Seconds

(without alignments)

5672.046 Million cell updates/sec

File: 08-08-906\_365-1

Perfect Score:

1686

Sequence: 1 cagccatctatctcttccatc.....aaagacccacagctctcagaa 1686

Scoring table:

IDENTITY.MD\*

Gapop 10.0 : Gapext 1.0

Searched: 7991742 seqs, 350374086 residues

Total number of hits satisfying chosen parameters: 15983484

Minimum hit seq length: 0

Maximum hit seq length: 200000000

Post processed: Maximum March 08

Listing first 45 summaries

Database:

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190: qb\_gss25:\*  
 191: qb\_gss26:\*  
 192: qb\_gss27:\*  
 193: qb\_gss28:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	173.4	10.3	531	4	AA224131	AA224131: 114407.1
2	157	9.3	782	40	AW134052	AW134052: 114407.1
3	155.4	9.2	641	97	AW76646	AW76646: EST148745
4	115.2	6.8	611	166	AG714125	AG714125: EST151218
5	99.8	5.9	908	109	BE546976	BE546976: 601071950
6	90.2	5.3	413	40	AW114877	AW114877: M6809
7	89.6	5.3	275	102	BA196485	BA196485: BA196485
8	88.2	5.2	462	7	AA11286	AA11286: 226403.1
9	88.2	5.2	477	19	AI341113	AI341113: 3384602.1
10	88.2	5.2	479	23	AI653235	AI653235: 3424204.1
11	88.2	5.2	549	28	AI612328	AI612328: 3424204.1
12	86.4	5.1	385	38	AV647429	AV647429: AV647429
13	86.4	5.1	399	38	AV647483	AV647483: AV647483
14	86.4	5.1	399	38	AV647486	AV647486: AV647486
15	86.4	5.1	446	19	AI362624	AI362624: 126410.1
16	86.4	5.1	465	22	AI393892	AI393892: 1405605.1
17	85.2	5.1	450	174	AG932574	AG932574: 8371.23-3
18	85.2	5.1	645	109	BE533846	BE533846: 601234423
19	84.8	5.0	384	12	AA651319	AA651319: EST194087
20	84.8	5.0	384	13	AA651319	AA651319: EST194087
21	84.8	5.0	390	146	WI3715	WI3715: m643604.1
22	84.8	5.0	128	18	AI323443	AI323443: m42464.1
23	84.8	5.0	451	19	AI327473	AI327473: m42464.1
24	84.8	5.0	509	91	AW460889	AW460889: 01-M-BH3-
25	84.8	5.0	574	17	AI171721	AI171721: EST127704
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34	82.2	4.9	431	111	BE655969	BE655969: 155233.1
35	82.2	4.9	1131	135	BE747494	BE747494: 601306416
36	81.6	4.8	264	102	BE196502	BE196502: BE196502
37	81	4.8	291	126	BE268780	BE268780: BE268780
38	79.4	4.7	941	191	CONS1491	CONS1491: 10174000
39	79.2	4.7	508	147	W55445	W55445: m456406.1
40	79.2	4.7	536	1	AA003987	AA003987: m456406.1
41	79.2	4.7	666	109	BE546759	BE546759: 601306416
42	79.2	4.7	823	199	CONS1491	CONS1491: 10174000
43	79	4.7	724	18	AI174742	AI174742: 0122609.1
44	79	4.7	972	135	BE737286	BE737286: 601307107
45	78.4	4.7	479	12	AA621160	AA621160: 0814739.5

## ALIGNMENTS

RESULT 1  
 LOCUS AA224131/c  
 DEFINITION 271602.11 StrataGene BIR reaction (477233) BIRCO captures cDNA clone  
 IMAGE:648794.57, mRNA sequence.  
 ACCESSION AA224131  
 VERSION AA224131.1 GI:1844690  
 KEYWORDS EST.  
 SOURCE human.



[illegible]

DB	574	ATAG	578																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
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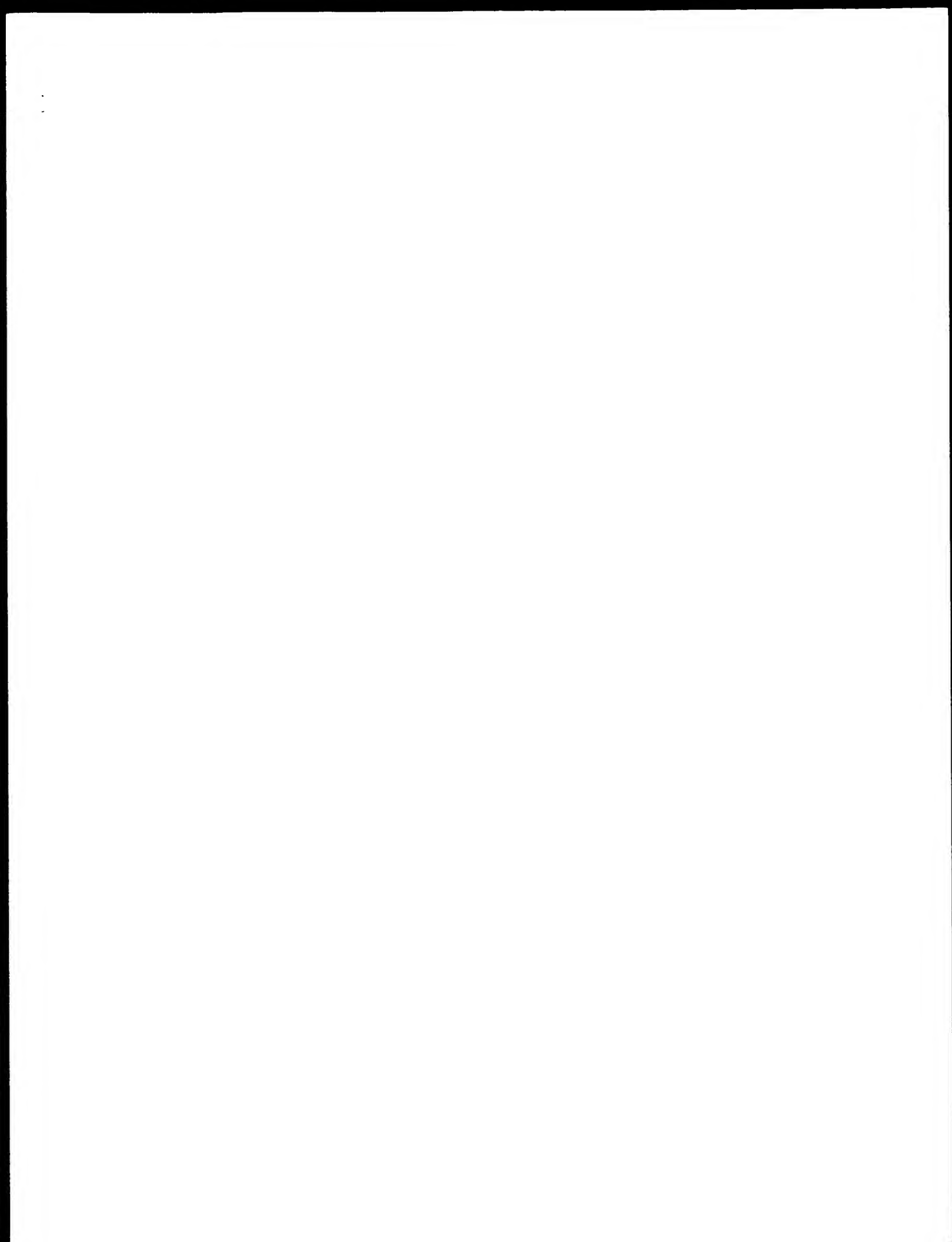


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us-08-906-365-1.rst

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Page 11









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1 APPLICATION NUMBER: GB 9518272.1
2 FILING DATE: 08-SEP-1995
3 PRIORITY APPLICATION DATA:
4 APPLICATION NUMBER: GB 9605550.4
5 FILING DATE: 15-MAR-1996
6 PRIORITY APPLICATION DATA:
7 APPLICATION NUMBER: GB 9607532.0
8 FILING DATE: 11-APR-1996
9 PRIORITY APPLICATION DATA:
10 APPLICATION NUMBER: GB 9609576.5
11 FILING DATE: 08-MAY-1996
12 INFORMATION FOR SEQ ID NO: 14:
13 SEQUENCE CHARACTERISTICS:
14 LENGTH: 484 amino acids
15 TYPE: amino acid
16 TOPOLOGY: linear
17 ORIGINAL SOURCE:
18 ORGANISM: Mus musculus
19 US-08-836-620A-14

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Query Match 80.6%; Score 2262; DB 2; Length 484;

Best Local Similarity 89.0%; Pred. No. 7,26-234; Matches 426; Conservative 23; Mismatches 35; Indels 0; Gaps 0;

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QY 1c KLVYSLAVNNTSLNSVINELESLSPVNLWPIPSHLSIVVHPLSHIYAFPSK 105
DB 1 MAFYSPAVNMYSPSTSLNTEGIVPOTASPNVLTSPSLSLPLAFCOSLITAYPDKS 60
QY 106 PWCENSLHTLVNPEETLKPKVSNPCSPVTPGSKPAPKAVCSYASVHYGVMS 165
DB 61 PWLEASLHTLVNPEETLKPKVSNPCSPVTPGSKPAPKAVCSYASVHYGVMS 120
QY 166 GGGGAFAFNSLGGHNYGPAINATLGNPKRSYATLNRATVYVWVKGSSKRLK 425
DB 121 GGGGAFAFNSLGGHNYGPAINATLGNPKRSYATLNRATVYVWVKGSSKRLK 180
QY --55 VLVHLEFALVLEFALVLEFALVLEFALVLEFALVLEFALVLEFALVLEF 285
DB 181 VLVHLEFALVLEFALVLEFALVLEFALVLEFALVLEFALVLEFALVLEF 240
QY 286 SALLFASMRSLALALALALALALALALALALALALALALALALALALALAL 345
DB 241 SALLFASMRSLALALALALALALALALALALALALALALALALALALALAL 300
QY 346 KSLDHRKSLFADLVLDHSGVGLDPLHMLATISKEEFTKIGHEVTVVAMU 405
DB 301 KSLDHRKSLFADLVLDHSGVGLDPLHMLATISKEEFTKIGHEVTVVAMU 360
QY 406 LNSSMPLVATQDAVSSEKRLAHLLNAVTDALVWVIAKSGTSSQGSMPRLANLMLSHV 465
DB 361 LNSSMPLVATQDAVSSEKRLAHLLNAVTDALVWVIAKSGTSSQGSMPRLANLMLSHV 420
QY 466 KASNSKMEHLNKRKAVVYVLLLLMLNAVTSCKKSKSTIGSESPFEDSKREGSQ 525
DB 421 KASNSKMEHLNKRKAVVYVLLLLMLNAVTSCKKSKSTIGSESPFEDSKREGSQ 480
QY 526 NNGS 525
DB 481 NNGS 484

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# RESULT 6

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1 US-08-836-620A-15
2 Sequence 15, Application US/08836620A
3 Patent No. 5958710
4 GENERAL INFORMATION:
5 APPLICANT:
6 TITLE OF INVENTION: Orphan receptor
7 NUMBER OF SEQUENCES: 19
8 COMPUTER READABLE FORM:
9 MEDIUM TYPE: Floppy disk
10 COMPUTER: IBM PC compatible

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1 OPERATING SYSTEM: PC-DOS/MS-DOS
2 SOFTWARE: Patent In Release #1.0, Version #1.25 (EPP)
3 CURRENT APPLICATION DATA:
4 APPLICATION NUMBER: US/08/836,620A
5 FILING DATE:
6 PRIORITY APPLICATION DATA:
7 APPLICATION NUMBER: PCT/EP96/04933
8 FILING DATE:
9 APPLICATION NUMBER: GB 9518272.1
10 FILING DATE: 08-SEP-1995
11 PRIORITY APPLICATION DATA:
12 APPLICATION NUMBER: GB 9605550.4
13 FILING DATE: 15-MAR-1996
14 PRIORITY APPLICATION DATA:
15 APPLICATION NUMBER: GB 9607532.0
16 FILING DATE: 11-APR-1996
17 PRIORITY APPLICATION DATA:
18 APPLICATION NUMBER: GB 9609576.5
19 FILING DATE: 08-MAY-1996
20 INFORMATION FOR SEQ ID NO: 15:
21 SEQUENCE CHARACTERISTICS:
22 LENGTH: 383 amino acids
23 TYPE: amino acid
24 TOPOLOGY: linear
25 ORIGINAL SOURCE:
26 ORGANISM: Homo sapiens
27 US-08-836-620A-15

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Query Match 71.9%; Score 2017; DB 2; Length 384;

Best Local Similarity 100.0%; Pred. No. 9,46-208; Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 46 LELVYHRLSLHLLALVLAFLVLAFLVLAFLVLAFLVLAFLVLAFLVLAFLV 145
DB 2 LELVYHRLSLHLLALVLAFLVLAFLVLAFLVLAFLVLAFLVLAFLVLAFLV 61
QY 146 AEECAVCSLVSAYSDVSWSEDESKATFESLGGHNYGPAINATLGNPKRSYAT 205
DB 62 AEECAVCSLVSAYSDVSWSEDESKATFESLGGHNYGPAINATLGNPKRSYAT 121
QY 206 LKCYTVSVKVGSPPEFVGVLEVGVLEVGVLEVGVLEVGVLEVGVLEVGVLE 265
DB 122 LKCYTVSVKVGSPPEFVGVLEVGVLEVGVLEVGVLEVGVLEVGVLEVGVLE 181
QY 266 LSVHLEFALVLEFALVLEFALVLEFALVLEFALVLEFALVLEFALVLEF 325
DB 182 LSVHLEFALVLEFALVLEFALVLEFALVLEFALVLEFALVLEFALVLEF 241
QY 326 DQVLESCMEVLMGLMPSLIDPCKLFAVDLVLDHSGVGLDPLHMLATIS 385
DB 242 DQVLESCMEVLMGLMPSLIDPCKLFAVDLVLDHSGVGLDPLHMLATIS 301
QY 386 EPEEIKLGGFYGVVAMTINSNMPLVATQDAVSSEKRLAHLLNAVTDALVWVIAK 445
DB 302 EPEEIKLGGFYGVVAMTINSNMPLVATQDAVSSEKRLAHLLNAVTDALVWVIAK 361
QY 446 ISSQGSMPRLANLMLSHVSHA 468
DB 362 ISSQGSMPRLANLMLSHVSHA 384

```

# RESULT 7

```

1 US-08-836-620A-17
2 Sequence 17, Application US/08836620A
3 Patent No. 5958710
4 GENERAL INFORMATION:
5 APPLICANT:
6 TITLE OF INVENTION: Orphan receptor
7 NUMBER OF SEQUENCES: 19
8 COMPUTER READABLE FORM:
9 MEDIUM TYPE: Floppy disk
10 COMPUTER: IBM PC compatible

```





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CURRENT APPLICATION DATA:
APPLICATION NUMBER: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/02088
FILING DATE: 28 JUN 1994
PRIORITY DATE: 28 JUN 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 110 298.2
FILING DATE: 28 JUN 1994
ATTORNEY/AGENT INFORMATION:
NAME: Murray, Robert B.
REGISTRATION NUMBER: 22,980
REFERENCE/WORK NUMBER: 6564-5019
TELEPHONE: (202) 638-5500
TELEFAX: (202) 638-4410
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 773 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
FEATURE:
NAME/KEY: Miscellaneous
LOCATION: (1-423)
OTHER INFORMATION: /note "PIP recombinase domain."
FEATURE:
NAME/KEY: Miscellaneous
LOCATION: (424-428)
OTHER INFORMATION: /note "linker peptide."
FEATURE:
NAME/KEY: Miscellaneous
LOCATION: (429-773)
OTHER INFORMATION: /note "Estrogen binding domain."
US-08-564-264-1

```

Query Match 28.9% Score 810; DB 3; Length 773;  
 Host Local Similarity 30.9%; Prod. No. 8,56-78;  
 Matches 108; Conserved: 41; Mismatches 120; Gaps 15;

```

5 NSPSGINSFSSYSGSSTLLEHNSLYPSVSDSHHEFYAFYSPAVMNSISNVN 64
278 NLVSYNALANNAVSYFAIKN-----FASHICK-----LMTSP-----LSKKGLTELIN 325
65 LRT-----GPKQITSPNWIPIPDH SPIVVRQI SHLYAEQKSPWCARSLHTL 117
426 VVGNMSKRAVAVARTYTHITAIPIHYFALV-----SKVYAYD----- 365
118 IHNRELEKRAVSGNRCASIV-----LQPSKRIAHCAVCS-- LVASQYHG 162
466 PLSKMIAIKQIN-----PIEFWGHLEQKSAKSGSIRIPANGIIISGLVLISSY--- 418
164 VWSFSSVAFSPSTIGMNYIPATNCTTKSGPPKSGAPFIPKRYTVGVWKGSSPP 222
419 -----INRISIV-----GSMKQIFED 436
243 KQYHLVGRKSAQDQWAVAKPSQDAQV-----ELLIALSP 491
447 KQVYKHLKRPQFQ-----GQCFVSAIIPASNIWSTLMINPSKNSLASLAW 491
267 QVVIPIIAPAPVYISF--PSAPTFASMMSTFPAKEI VHI SWAKIPIQVFI 524
442 QVYVATIAAPQ IYSYVPIIPSPASMMG IENAIPEI VHI WAKFVQCFVFI 550
445 EVYVATIAWQVIMMIMMSSTIPIPIIPAPV VILFEGKQVFGILETFLMILAT 384
551 HGVVHIPIVAFIPIIMINWVMSKPIVAILPAPNIIIPNQGKPVGVVFIPIMLATS 610
446 SPGRKIKRKYIVKAMITINSMPPIVAT--GTAQSSPTAHINAVTIAI WVIAT 443
611 SPGRKIKRKYIVKAMITINSMPPIVAT--GTAQSSPTAHINAVTIAI WVIAT 443

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444 SLSGSAVQVAFIPIIIPVGRKSAQDQWAVAKPSQDAQV-----ELLIALSP 491
671 ACTTGVWQVAFIPIIIPVGRKSAQDQWAVAKPSQDAQV-----ELLIALSP 491

```

RESULT 12  
 US-08-693-940-3  
 Sequence 3, Application US/0869940  
 Patent No. 613027  
 ORIGINAL INFORMATION:  
 APPLICANT: Yee, Jiling-Kuan  
 APPLICANT: Pichman, Theodore  
 APPLICANT: Chen, Shun-Tai  
 TITLE OF INVENTION: Inducible Expression System  
 TITLE OF INVENTION: Inducible Expression System  
 TITLE OF INVENTION: Inducible Expression System  
 NUMBER OF SEQUENCES: 3  
 CORRESPONDENCE ADDRESS:  
 STREET: 285 Hamilton Ave., Suite 200  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94301  
 COMPUTER REWARDABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/693,940  
 FILING DATE: 07-AUG-1996  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Francis, Carol L.  
 REGISTRATION NUMBER: 46,513  
 TELEPHONE/TELEFAX NUMBER: 6510-055001  
 TELEPHONE: 650-327-3400  
 TELEFAX: 650-327-3231  
 INVENTION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 651 amino acids  
 TYPE: amino acid  
 STRANDINESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-693-940-3

Query Match 27.2% Score 742; DB 3; Length 611;  
 Host Local Similarity 59.1%; Prod. No. 96-73;  
 Matches 143; Conserved: 57; Mismatches 48; Gaps 1;

```

242 ALSPGATLILFALQVILNIP--GAV--EAVRMS--E--AKK--VHNS--SWAKIPIQ 419
416 SIIVAVVAVIADVQV IYVYVYVQVQVQVAV--GMS--V--QV--QV--QV--QV 423
423 VLSLLEKPLLESIMVWMM--LMM--S--H--G--E--A--V--G--V--G--V--G--V 479
424 VLSLLEKPLLESIMVWMM--LMM--S--H--G--E--A--V--G--V--G--V--G--V 483
720 IATLEFETIIGVHIVVAVAMIN--NS--MP--VAT--GTAQSSPTAHINAVTIAI 438
484 IATSPHMMNIGTFVQV--K--G--N--V--V--V--V--V--V--V--V--V--V 443
449 WVIAT--S--S--S--S--S--S--S--S--S--S--S--S--S--S--S--S--S 408

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Db 544 HUMAKAGLILQOQROHQLACILLLSHIRMSKGMEEHYSMKCKNVVPLDLEMLDAH 603
QY 499 VL 500
Db 604 RL 605

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RESULT 14
US-08-836-620A-9
: Sequence 9, Application US/08/836,620A
: Patent No. 5958710
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: Orphan receptor
: NUMBER OF SEQUENCES: 19
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/836,620A
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/EP96/03933
: FILING DATE:
: APPLICATION NUMBER: GB 9518272.1
: FILING DATE: 08-SEP-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9605550.4
: FILING DATE: 15-MAR-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9607532.0
: FILING DATE: 11-APR-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9609576.5
: FILING DATE: 08-MAY-1996
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 243 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: ORIGINAL SOURCE:
: ORGANISM: Mus musculus
: US-08-836-620A-9

```

```

Query Match 23.88; Score 668.5; DP 2; Length 243;
Best Local Similarity 54.94; Pred. NO. 1.8e-63;
Matches 124; Conservative 52; Mismatches 49; Indels 1; Gaps 1;

QY 405 ELVHIMISAKKIPGVFVSLIDVOVLLSCMVEVIMGLMMPSTDPKTEFAPDLVDR 364
Db 1 ELVHIMINAKRVPGRGDLNIDQVHLLCCANLELMIGLVMSMEHPCKLLFAPDLDR 60
QY 465 DEKRVGCTETFTMLATTSRPFELKIQHKEYLCVKAMILLNSMPLVATF QDADSS 423
Db 61 NQGRKVPQVETFTMLATTSRPFPMNIGPFFVTKSTIIINSVYFTLSSTLKSLEK 120
QY 424 KRIAMHNAVVTAVVWIAKSTISQAGSMFTANIMLSHVHASNCGMELLNMCKKN 483
Db 121 DHIRVATKIDILHMAKANLITDOOHRRLAQLLLSHIRMSNGMEHLYNMCKKN 180
QY 484 VVIVYDILLEMNAHVLNPGKSSITGSPSPAEISKSKESQNPQS 529
Db 181 VVPLVDLLEMLDRIHAPASPMVPPPEPSQTGLATSTSAHS 226

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```

RESULT 14
US-08-836-620A-8
: Sequence 8, Application US/08836620A
: Patent No. 5958710

```

```

: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: Orphan receptor
: NUMBER OF SEQUENCES: 19
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/836,620A
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/EP96/03933
: FILING DATE:
: APPLICATION NUMBER: GB 9518272.1
: FILING DATE: 08-SEP-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9605550.4
: FILING DATE: 15-MAR-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9607532.0
: FILING DATE: 11-APR-1996
: APPLICATION NUMBER: GB 9609576.5
: FILING DATE: 08-MAY-1996
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 243 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: ORIGINAL SOURCE:
: ORGANISM: Rattus rattus
: US-08-836-620A-8

```

```

Query Match 23.74; Score 665; DP 2; Length 243;
Best Local Similarity 56.94; Pred. NO. 3.4e-63;
Matches 124; Conservative 50; Mismatches 40; Indels 4; Gaps 2;

QY 305 ELVHIMISAKKIPGVFVSLIDVOVLLSCMVEVIMGLMMPSTDPKTEFAPDLVDR 364
Db 1 ELVHIMINAKRVPGRGDLNIDQVHLLCCANLELMIGLVMSMEHPCKLLFAPDLDR 60
QY 365 DEKRVGCTETFTMLATTSRPFELKIQHKEYLCVKAMILLNSMPLVATF QDADSS 423
Db 61 NQGRKVPQVETFTMLATTSRPFPMNIGPFFVTKSTIIINSVYFTLSSTLKSLEK 120
QY 424 KRIAMHNAVVTAVVWIAKSTISQAGSMFTANIMLSHVHASNCGMELLNMCKKN 483
Db 121 DHIRVATKIDILHMAKANLITDOOHRRLAQLLLSHIRMSNGMEHLYNMCKKN 180
QY 484 VVIVYDILLEMNAHVLNPGKSSITGSPSPAEISKSKESQNPQS 529
Db 181 VVPLVDLLEMLDRIHAPASPMVPPPEPSQTGLATSTSAHS 226

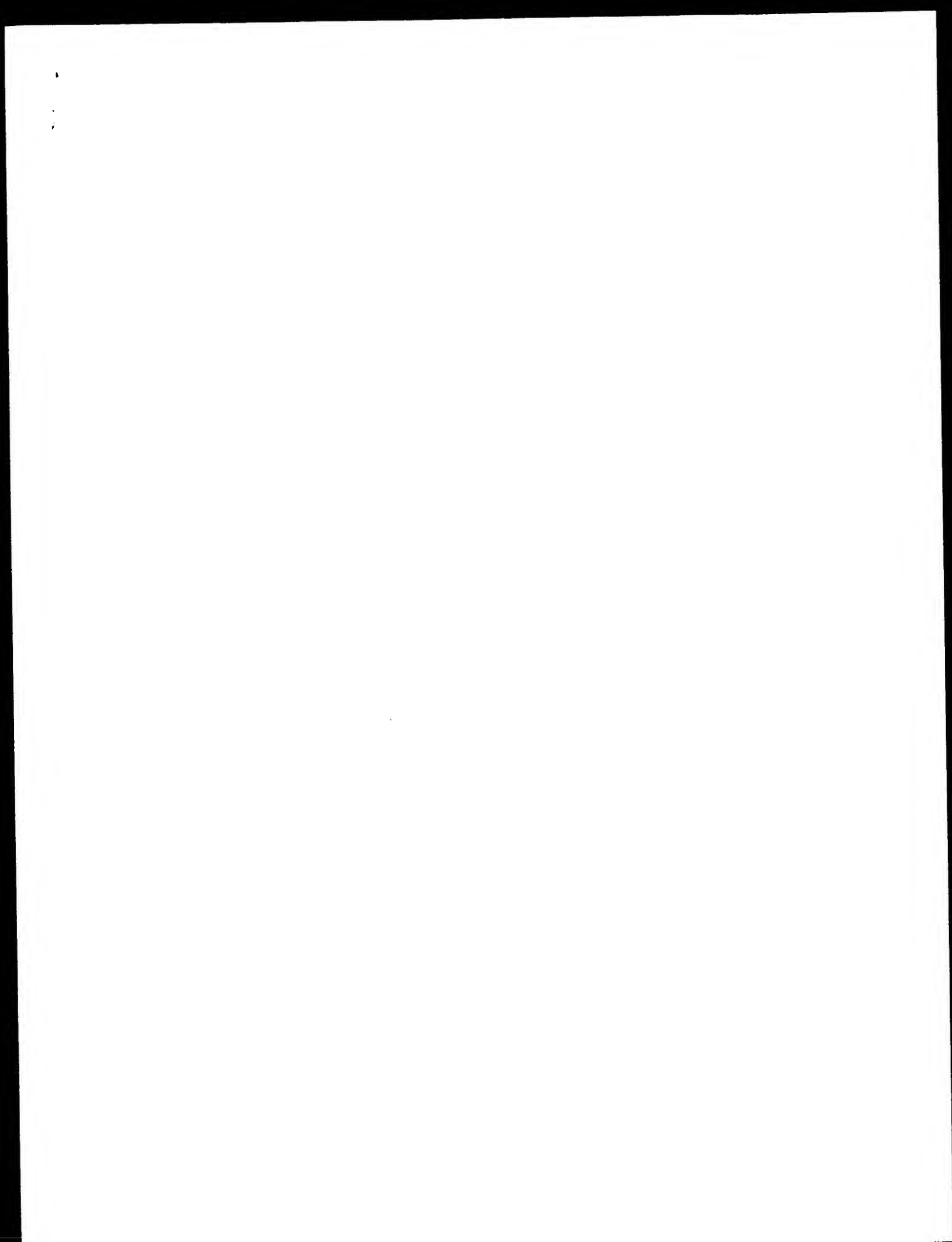
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RESULT 15
US-08-836-620A-10
: Sequence 10, Application US/08836620A
: Patent No. 5958710
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: Orphan receptor
: NUMBER OF SEQUENCES: 19
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/836,620A
: FILING DATE:

```

















10 525 MSHFVQNF TAAVITVLTLMAMHSDHGVAVLNSVAVSLPSSLSQVLAHVS 584  
 27 577 GRSSTFSGW 747  
 14 585 LSASHKEESH 595

## RESULT 11

564737  
 408 Oestrogen receptor - human  
 (Species: Homo sapiens (man))  
 CDate: 28 Oct 1995 #sequence\_revision 13 Mar 1997 #cdat\_change 20 Aug 1999  
 Accession: S64737  
 RefSeq: J03703; Mol: D.M.: Billmoria, M.M.: Jordan, V.C.  
 Nucleic Acids Res. 24: 962-969, 1996  
 A title: A novel 80 kDa human estrogen receptor containing a duplication of exons 6 and  
 A accession number: S64737; MIM:39174665  
 A residues: 564737

Accession: preliminary nucleic acid sequence not shown; translation not shown  
 A molecule type: mRNA

A residues: 1-701 -> 141

A cross-reference: EMBL:U47676; NID:q197854; PIN:AA00115.1; PID:q197855

A note: The nucleic acid sequence was submitted to the EMBL Data Library, January 1996  
 C keywords: estrogen receptor; ova transforming protein homology

F104-456/omai: ova transforming protein homology (ERBA)

F104-562/omai: ova transforming protein homology (ERBA)

Query Match 41.0% Score 174.5; DB 2; Length 701;

Best local similarity 41.2% Prod. No. 5,70-84;

Matches 299; Overlap: 47; Mismatches 125; Indels 171; Gaps 16;

07 5 NISNSNSSTSYNSQSLILHL GSYITSS YVSHHYEYAMFYSAVMNYSIPS 60  
 14 21 NLELELN-----QKKEFEPLEVEYLLSKPAVYNYEGAAVEENAAVAAYG 74  
 07 61 NVNLELNQGP-----TSPNWLTPCHLSP-LVHROLSHLAE 101  
 14 75 V LLLVYDSSAAKSNGLDHPPLNSVSLMLHPPLSPFLQVPOQVPPYLE 133  
 07 102 PGRSW-----FARLEHLPVREHLPKRVSONGASPYTPG-----SKQAHFCVSSD 154  
 14 114 NPSYIVAEAPVAPVPP-----NSDNPQGPPLASTNDKSNMASEKKEITPVAVCD 190  
 07 155 VASQHYVWNSPCKAKPKKSTGSHNYTQATWGLTKRBSQACGLPKCYEVM 214  
 14 191 VASQHYVWNSQKPKKSTGSHNYTQATWGLTKRBSQACGLPKCYEVM 250  
 07 215 VPSPEPPEVPLVPPGSAFEGTCAGKAPRSGSHAPV-----EL 258  
 14 251 MKGQIKRQKQKRLKMKKQKRD-----GKQKEVGSADMDMAANWPSPLMKSKNS 305  
 07 259 LLAASPTGVITTFAPGVHLSR-PSAFTFASMMKSTIKLAPLVMISMAK 316  
 14 305 LALSTFAMMSALIFAPFP-PIVYFPTPTFSLAMGLITLADRELVMIMAKV 364  
 07 377 PPSVSTPEVPLTFEYVWGLWPSLHBEKLFAPLVLPDCEYCGVLEI 376  
 14 405 PPSVSTPEVPLTFEYVWGLWPSLHBEKLFAPLVLPDCEYCGVLEI 424  
 07 477 FEMLATISAPPEIKLGRFYVAVAMLLNSMYLVIAF-----GQ 419  
 14 425 FEMLATISAPPEIKLGRFYVAVAMLLNSMYLVIAF-----GQ 484  
 07 429 -----ADSR----- 424  
 14 485 LILHMAKAGLLGQGHPLAALLLSHIRMNGKQVEQVELFOMLATISSPRM 544  
 07 425 -----KLHLNAVDPAVWLAKSISQ 449  
 14 545 NQDHEVWLSITITNSVWTFSSITKSPFGQHHVLPFTTTTTHMAKASTT 604

07 477 FEMLATISAPPEIKLGRFYVAVAMLLNSMYLVIAF-----GQ 419  
 14 425 FEMLATISAPPEIKLGRFYVAVAMLLNSMYLVIAF-----GQ 484

## RESULT 12

558224  
 Oestrogen receptor Atlantic salmon (Atlantic salmon)  
 (Species: Salmo salar (Atlantic salmon))  
 CDate: 13-Jan-1996 #sequence\_revision 01 Mar 1996 #cdat\_change 20 Aug 1999  
 Accession: S58224  
 RefSeq: S.A.: Billmoria, M.M.: Jordan, V.C.: 1996  
 Submitted to the EMBL Data Library, July 1996

A accession number: S58224

A reference number: S58224

A status: preliminary

A molecule type: mRNA

A residues: 1-545 -> 100

A cross-reference: MIM:390656; NID:q197854; PIN:AA00115.1; PID:q197855

A note: The nucleic acid sequence was submitted to the EMBL Data Library, July 1996

C keywords: steroid hormone receptor; ova transforming protein homology

F104-482/omai: ova transforming protein homology (ERBA)

Query Match 40.4% Score 134.5; DB 2; Length 545;

Best local similarity 40.8% Prod. No. 5,40-81;

Matches 259; Overlap: 94; Mismatches 113; Indels 71; Gaps 15;

07 70 GQQLSPNVLWIDHSHLVVHLESH-----LYAHFKSTWFAVSEHLPVNEH 125  
 14 17 NSPTGIVVSSVYLSLF LHTFHHNLSVSYLSSTSTVSSVNLNLSH 174  
 07 124 LKKVSONGAS-PVTPGSK-----KQAHVAVSGAS-IRVWNS-CKKAKKST 177  
 14 75 -KQITTSNLSVAAAGSVAVEMANIRVAVVSGAS-VAVWNS-CKKAKKST 193  
 07 178 GSHNYTQATWGLTKRBSQACGLPKCYEVMVWNSQSHBEKLPVPSAL 207  
 14 144 GSHNYTQATWGLTKRBSQACGLPKCYEVMVWNSQSHBEKLPVPSAL 217  
 07 218 QHHC-ACKAKR-----SSSH-APVQLILALNSF 248  
 14 188 KPVGPAHDEFRVYDLPHTAPGQDPPSSSSSSSSGAGWQD 300  
 07 269 VALLAHFVGLSFG-----SALFLASMMKSLKLAQKLVMTMAKATLVIT 276  
 14 242 LFLCAAPF-AISPVKAPVYIVIMLILSMAKLVIMVIAKRVV-CHLSH 300  
 07 327 QVLETSVMEVIMMIMKSHHBEKLFAPLVLPDCEYCGVLEI 376  
 14 401 QVLETSVMEVIMMIMKSHHBEKLFAPLVLPDCEYCGVLEI 424  
 07 497 PPSVSTPEVPLTFEYVWGLWPSLHBEKLFAPLVLPDCEYCGVLEI 424  
 14 461 PPSVSTPEVPLTFEYVWGLWPSLHBEKLFAPLVLPDCEYCGVLEI 484  
 07 446 LNSQSMELANLMLSTVHASNQMGELNMK-KNVYVYVLELMNAVLPK 476  
 14 421 ASVQGPPEVPLTFEYVWGLWPSLHBEKLFAPLVLPDCEYCGVLEI 476  
 07 596 STTDSQSAHDEKSLNSG-NQS 529  
 14 477 -----SHKVAQAEQTEQST 495  
 07 596 STTDSQSAHDEKSLNSG-NQS 529  
 14 477 -----SHKVAQAEQTEQST 495

## RESULT 13

A47197  
 estrogen receptor rainbow trout  
 (Species: Oncorhynchus mykiss (rainbow trout))  
 CDate: 31-Jan-1992 #sequence\_revision 1 Jan 1992 #cdat\_change 20 Aug 1999  
 Accession: A47197; MIM:40070  
 RefSeq: F. Le Gac, F. Le Gac, P. Vernet, Y.  
 Mol. Cell. Endocrinol. 71: 195-204, 1990

A>Title: Full length sequence and in vitro expression of rainbow trout estrogen receptor  
 A:Accession number: AF7197; MIM:1006624  
 A:Accession: A37197  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-574 <1K>  
 A:Cross-references: GB:X51454  
 A:Keywords: DNA binding; nuclear; steroid hormone receptor; transcription regulation; zinc finger  
 F145-427/Region: cDNA transforming protein homology  
 F147-167/Region: zinc finger  
 F183-207/Region: zinc finger

Query Match 49.9%; Score 1120; DB 2; length 574;  
 Best Local Similarity 48.8%; Pred No. 1-80;  
 Matches 243; Conservative 70; Mismatches 127; Indels 58; Gaps 12.

QY 70 GGGTSPNVVWPTGHSNVLV---VHQLSH-----LYAEPOKSWCAEHLHTLPVN 120  
 DB 55 GSSPGGFLVSSSPQLSDPSFLPPSHHGLPSQSYLETSLPPLYSVVNTOLSA 114  
 QY 121 EELL---KEVSGEAGVPTGPTSKELAECAVGEVAGVGVGSCGKAEFKS 176  
 DB 115 EKKICLASHKQSGVAGVAFEMANTRYCAVSDPAGSYHGVGSCGKAEFKS 174  
 QY 177 IGVHNVVTPATNGTTFNPPSSQAVPLPGVEVDMKSSPEHGVPLVPR----- 231  
 DB 179 IGVHNVVTPATNGTTFNPPSSQAVPLPGVEVDMKSSPEHGVPLVPR----- 231  
 QY 212 -----GVANDEGHCAQAKARSSG--HAPVPEHLDAISPPQVLTILE 274  
 DB 214 GHAAPPEPTVWSTQDQVTPNPSSTLNGGVWMPPT-----TPPPQ-VLPLQ 286  
 QY 275 APPHVIISRP--SAPPTFASMMMSLTKLADKELVHMTSMARKIDPEVLSLEDQVILE 332  
 DB 287 GGTTP-AICSKQKVARVYETVIMTLLTSMADKELVHMTSMARKVGHQFSLDQVILE 345  
 QY 333 GVMVVIWMLMPSTPHGKTIIPAPNVLPHPGKGVCTIFTPMLLATSPPELKL 392  
 DB 346 SSMLEVLMLGLWSTHCPKLEFADLLDRSEGVVGMATPMLLATVSRFQMLKL 405  
 QY 393 QREKELVYKAMILLNSSMPLVLT-ATQDASSKLAHLNAVDAVWIAKSGISSQOO 451  
 DB 406 KPEEVGCKAILLLNGCAFSPGNSVESLHNSAVESMLDITDALIHHSISASVQGO 465  
 QY 463 SGRRLMLLMLSHVSHARKVPHLNRKRVNVVYDLEMLNAVHPGKSSITGSE 511  
 DB 466 PRQADLLTLLSHIKMSKMKMBHYSLKPKVPIYPILEMLDHPQ----- 515  
 QY 512 GSTAHSKSGESGNS 529  
 DB 516 -APGVACAGDETGST 532

RESULT 14  
 B29345  
 steroid hormone receptor ERK precursor - human  
 C:Species: Homo sapiens (man)  
 C:Date: 15-Nov-1998  
 C:Accession: B29345  
 C:Accession: B29345  
 C:Keywords: V. Yang, N. Soudi, P. Franz, E.M. Nature 311, 91-94, 1998  
 A>Title: Identification of a new class of steroid hormone receptors.

A:Reference number: A29345; MIM:83123546  
 A:Accession: B29345  
 A:Molecule type: mRNA  
 A:Residues: 1-433 <1K>  
 A:Cross-references: GB:X51417, MIM:836610, PDB:1AA5779.1, PDB:436611, PDB:Y00290  
 A:Keywords: DNA binding; steroid hormone receptor; transcription regulation; zinc finger  
 F103/352/Region: cDNA transforming protein homology  
 F103/133/Region: zinc finger  
 F133-163/Region: zinc finger

Query Match 52.5%; Score 615; DB 2; length 433;  
 Best Local Similarity 33.5%; Pred No. 9-42;  
 Matches 173; Conservative 78; Mismatches 147; Indels 119; Gaps 19;

QY 3 IKNSTSLNLSNYSNWSLPLELHSLYLSYVPSHHTFAMLYSVAVMYSTPS 60  
 DB 26 ITERS-----PSGIALSHHS-----PS 46  
 QY 61 NVIN-EGTGGT-LSNVWVPTGHSNVLV---VHQLSH-----LYAEPOKSWCAEHLHTLPVN 117  
 DB 37 GSSDAGGFGMALGIHANTHSHMPAG-----AGAGNPKSKSYHCHISGIMED-- 86  
 QY 118 PNVPELTKPVSNP-----ASPV-TPSSQVAGVGVGSCVAVGVGSCGKAE 172  
 DB 87 -----SAKCEVNLNP-----KR---LALVGGIASHYHGVAGVAGVAGVAGV 126  
 QY 173 PPSGIDQVWVPTGHSNVLV---VHQLSH-----LYAEPOKSWCAEHLHTLPVN 230  
 DB 127 EKKICLASHKQSGVAGVAFEMANTRYCAVSDPAGSYHGVGSCGKAEFKS 186  
 QY 231 GQSNAPDGHCAQAKARSSG--HAPVPEHLDAISPPQVLTILE 285  
 DB 187 PPSGIDQVWVPTGHSNVLV---VHQLSH-----LYAEPOKSWCAEHLHTLPVN 229  
 QY 286 -SAPPTFASMMMSLTKLADKELVHMTSMARKIDPEVLSLEDQVILE 344  
 DB 230 DVPEDGILKLTTCGLAPPELVPLSMKHLPSNSLNGVMSLGVAMHLLIGIV 289  
 QY 345 WSTHHPGKTIIPAPNVLPHPGKGVCTIFTPMLLATSPPELKL 404  
 DB 290 YPSLYDKLAVAEVIMDEHSLV-GLDLYPAHLYGVKRLVRLVRLVRLVRLVRLV 348  
 QY 405 LNS SMPLVATLHNSMPLVLT-ATQDASSKLAHLNAVDAVWIAKSGISSQOO 462  
 DB 349 LANSLSM-----LENLEAVQKGLTFEALGVYI-----SQHPEHFAKSLITL 396  
 QY 463 SHVRAKNGMEHLNMKCKNVVYDLEMLNAVH 499  
 DB 397 PLRQTAARAVGHFYSVKDGVPMKLEMLEAKV 433

RESULT 15  
 S58087  
 estrogen receptor related protein - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 13-Jan-1996  
 C:Accession: S58087  
 C:Accession: S58087  
 C:Keywords: V. Yang, N. Soudi, P. Franz, E.M. Nature 311, 91-94, 1998  
 A>Title: Identification of a new class of steroid hormone receptors.

Query Match: 221K Score 619.50 DB Z: Length 433;  
 Best Local Similarity: 44.08; Pval: No; 86-41;  
 Matches: 170; Positives: 66; Mismatches: 144; Indels: 115; Gaps: 20;

```

01 1KNHGSINSSSTNSSTLLEHISYITSSYVD--SHHEYPAMIFYSYAVMNYSTPS 60
02 10 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
03 10 1KTFSS-----SSSLIALSHS-----PS 36
04 61 NVINEDDNY-RQITSPNWMPTSHESPLVVRQLSHLYAEPOKSPW--CEARSLHTL 117
05 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
06 47 SSIVASSDPEQIALSHAMILLSPREFA-----AGIGGPKCKSEYEDCTSGIMED-- 86
07 118 EVNNFELLKPKYS-NE-----ASTVEGDSKREHAFPAVNSLYASGYHYCVMSGCKCAAF 172
08 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
09 47 -SARKPEYMLNAP-----KR--DLVCGDIASGYHYGVASCEACRAAF 126
10 173 EPPSLDHNLYTANNGTIFVNPPEQZATLKKCYEVSXVKGSSP--EPPGYEPLVF 240
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
12 127 EPHLLGYNIVNVAINDTIFVPPSSGAVPPMPTPVQMKFQSVPLKVPKQKPKR 186
13 241 KQSKAP-----GQVQVAFPSGSHAPVPELILIALSPCEVL;LLEVEYHVLISPS 286
14 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
15 187 BRIDSENSPYINIPISPAKRP-----LKIVSNLIVEQ--DKLYAMPN-----D 231
16 287 APTIFASMMSLIKLAKEIVHMLISMARRIPQPVETSLFDQVRLLESQNMVEYLMGIMKR 346
17 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
18 242 IPBBIKAITTICPLAQELVPLINMARHIPPSPSTLIGQMSLQSSAMMETLILCIYKR 291
19 447 STDHNRKLIAPQGVLDQDEKRVGILIEFLMLAITTSREFELKLOHKEYLGVKAMILL 406
20 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
21 292 SLFYBOKLAVADYIMQEHKRLVGLIDHYRAIIQIVKRYKKLVKKEFEMLKALALA 350
22 407 NS-SMYPLVIALQADNSKRLAHLN-AVTIALVWVIKSGTSSQGSMTANILMLLSH 464
23 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
24 451 NSDSMY-----TENEEVQKLOLILHEALQVEL-----SQREHPRRACKLIMTLPL 498
25 465 VRIASNRIDREHLNMRCKNVVAVYDILEMLNABV 499
26 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
27 499 LKQIDAKAVGQVSVVQVWMLLEMLLAAV 443

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Search completed: April 19, 2001, 06:44:59  
 Job Time: 644 sec

1

2

3



Matches: 489; Conservative: 229; Mismatches: 20; Indels: 0; Gaps: 0

27 1 MDIKRSGSSLSRSTGSGSSSLA LKNGSIV LSSVDSHNEYVAMLPYSAVANNSTPS 60  
 1 MDIKRSGSSLSRSTGSGSSSLA LKNGSIV LSSVDSHNEYVAMLPYSAVANNSTPS 60

Db 1 MDIKRSGSSLSRSTGSGSSSLA LKNGSIV LSSVDSHNEYVAMLPYSAVANNSTPS 60

QY 61 NVRNRCGQNGQNTGQNVNMTTQNH SPVNVHQSLSTYAPKQSWCKAKSLPHLPVN 120  
 61 SVNLEHGRPRQITSPMLNSTGHSLPLAVHQLSHLVAPQKSWCEAPSEHLTPVS 120

Db 61 NVRNRCGQNGQNTGQNVNMTTQNH SPVNVHQSLSTYAPKQSWCKAKSLPHLPVN 120

QY 121 KETLKRRKVSNGSASVVTGSGSKTALEFVAVSDASVYHGVWSVDEYKAFKPSIQH 180  
 121 KETLKRRKVSNGSASVVTGSGSKTALEFVAVSDASVYHGVWSVDEYKAFKPSIQH 180

Db 121 KETLKRRKVSNGSASVVTGSGSKTALEFVAVSDASVYHGVWSVDEYKAFKPSIQH 180

QY 181 NDIYCEATNCTIDKNEKSGACPLFVEVAVGVSPPPEPQVPLVRGQNADEQLH 240  
 181 NDIYCEATNCTIDKNEKSGACPLFVEVAVGVSPPPEPQVPLVRGQNADEQLH 240

Db 181 NDIYCEATNCTIDKNEKSGACPLFVEVAVGVSPPPEPQVPLVRGQNADEQLH 240

QY 241 CAGKAKRSQGHAPRVRELLDALSPQIVLLEAFPHVLISRPASPTFASMMMSLTK 300  
 241 CAGKAKRSQGHAPRVRELLDALSPQIVLLEAFPHVLISRPASPTFASMMMSLTK 300

Db 241 CAGKAKRSQGHAPRVRELLDALSPQIVLLEAFPHVLISRPASPTFASMMMSLTK 300

QY 301 LAKELVHMTSMARKIPGEVELSLFDQVRLTESGMFVIMMGLMWRSTDPGKLIFAPDL 360  
 301 LAKELVHMTSMARKIPGEVELSLFDQVRLTESGMFVIMMGLMWRSTDPGKLIFAPDL 360

Db 301 LAKELVHMTSMARKIPGEVELSLFDQVRLTESGMFVIMMGLMWRSTDPGKLIFAPDL 360

QY 361 VLECEKQVESEITETMLATTSFEELKSGHELVKAMLLNSMYPLVATQGA 420  
 361 VLECEKQVESEITETMLATTSFEELKSGHELVKAMLLNSMYPLVATQGA 420

Db 361 VLECEKQVESEITETMLATTSFEELKSGHELVKAMLLNSMYPLVATQGA 420

QY 421 DSGRKLTHLLNAVTDALVWVIAKSGISSQGSQKRAVLMILSHVHASKCKEHLINMK 480  
 421 DSGRKLTHLLNAVTDALVWVIAKSGISSQGSQKRAVLMILSHVHASKCKEHLINMK 480

Db 421 DSGRKLTHLLNAVTDALVWVIAKSGISSQGSQKRAVLMILSHVHASKCKEHLINMK 480

QY 481 CRNVAVVYDILLFMNAHVIFGKSSITSGSPADSKSGESQNDPS 529  
 481 CRNVAVVYDILLFMNAHVIFGKSSITSGSPADSKSGESQNDPS 529

Db 481 CRNVAVVYDILLFMNAHVIFGKSSITSGSPADSKSGESQNDPS 529

RESULT 2

Q9XSH5 PRELIMINARY: PRI: 527 AA.

AC Q9XSH5; 01-NOV-1999 (TREMBLREL. 12, Created)

DT 01-NOV-1999 (TREMBLREL. 12, last sequence update)

DT 01-OCT-2000 (TREMBLREL. 15, last annotation update)

DE ESTROGEN RECEPTOR-BETA.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

OX NCBI\_TaxID:9913;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BRED HOLSTEIN; TISSUE-OVARIAN FOLLICLE;

KX Molecule C.S., Yuan X., Manikkam M., Calder M.D., Garverick H.A., Tashir D.B.;

RA "Cloning, sequencing, and localization of bovine estrogen receptor-beta within the ovarian follicle";

RT -; SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

DR EMBL: AF110402; AAD24432.1; -

DR HSSP: P03372; IHCP.

DR INTERPRO: IPR000324; -

DR INTERPRO: IPR000324; -

DR INTERPRO: IPR001628; -

DR PFAM: PF00104; hormone\_rec; 1.

DR PRINTS: PR00047; STRUTDFINCR.

DR PRINTS: PR00450; VITAMINOR.

DR PROSITE: PS00041; NUCLEAR\_RECEPTOR; 1.

KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;

QY 61 NVRNRCGQNGQNTGQNVNMTTQNH SPVNVHQSLSTYAPKQSWCKAKSLPHLPVN 120  
 61 SVNLEHGRPRQITSPMLNSTGHSLPLAVHQLSHLVAPQKSWCEAPSEHLTPVS 120

Db 61 NVRNRCGQNGQNTGQNVNMTTQNH SPVNVHQSLSTYAPKQSWCKAKSLPHLPVN 120

QY 121 KETLKRRKVSNGSASVVTGSGSKTALEFVAVSDASVYHGVWSVDEYKAFKPSIQH 180  
 121 KETLKRRKVSNGSASVVTGSGSKTALEFVAVSDASVYHGVWSVDEYKAFKPSIQH 180

Db 121 KETLKRRKVSNGSASVVTGSGSKTALEFVAVSDASVYHGVWSVDEYKAFKPSIQH 180

QY 181 NDIYCEATNCTIDKNEKSGACPLFVEVAVGVSPPPEPQVPLVRGQNADEQLH 240  
 181 NDIYCEATNCTIDKNEKSGACPLFVEVAVGVSPPPEPQVPLVRGQNADEQLH 240

Db 181 NDIYCEATNCTIDKNEKSGACPLFVEVAVGVSPPPEPQVPLVRGQNADEQLH 240

QY 241 CAGKAKRSQGHAPRVRELLDALSPQIVLLEAFPHVLISRPASPTFASMMMSLTK 300  
 241 CAGKAKRSQGHAPRVRELLDALSPQIVLLEAFPHVLISRPASPTFASMMMSLTK 300

Db 241 CAGKAKRSQGHAPRVRELLDALSPQIVLLEAFPHVLISRPASPTFASMMMSLTK 300

QY 301 LAKELVHMTSMARKIPGEVELSLFDQVRLTESGMFVIMMGLMWRSTDPGKLIFAPDL 360  
 301 LAKELVHMTSMARKIPGEVELSLFDQVRLTESGMFVIMMGLMWRSTDPGKLIFAPDL 360

Db 301 LAKELVHMTSMARKIPGEVELSLFDQVRLTESGMFVIMMGLMWRSTDPGKLIFAPDL 360

QY 361 VLECEKQVESEITETMLATTSFEELKSGHELVKAMLLNSMYPLVATQGA 420  
 361 VLECEKQVESEITETMLATTSFEELKSGHELVKAMLLNSMYPLVATQGA 420

Db 361 VLECEKQVESEITETMLATTSFEELKSGHELVKAMLLNSMYPLVATQGA 420

QY 421 DSGRKLTHLLNAVTDALVWVIAKSGISSQGSQKRAVLMILSHVHASKCKEHLINMK 480  
 421 DSGRKLTHLLNAVTDALVWVIAKSGISSQGSQKRAVLMILSHVHASKCKEHLINMK 480

Db 421 DSGRKLTHLLNAVTDALVWVIAKSGISSQGSQKRAVLMILSHVHASKCKEHLINMK 480

QY 481 CRNVAVVYDILLFMNAHVIFGKSSITSGSPADSKSGESQNDPS 529  
 481 CRNVAVVYDILLFMNAHVIFGKSSITSGSPADSKSGESQNDPS 529

Db 481 CRNVAVVYDILLFMNAHVIFGKSSITSGSPADSKSGESQNDPS 529

RESULT 3

Q9T015 PRELIMINARY: PRI: 527 AA.

AC Q9T015; 01-MAY-2000 (TREMBLREL. 13, Created)

DT 01-MAY-2000 (TREMBLREL. 13, last sequence update)

DT 01-OCT-2000 (TREMBLREL. 15, last annotation update)

DE ESTROGEN RECEPTOR-BETA.

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.

OX NCBI\_TaxID:9940;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-OVARY;

RA Cardenas H., Hingdy R.M., Foye W.P., Nephew K.P.;

RT "Cloning and expression of estrogen receptor beta in the ovine ovary";

RT submitted (AUG-1999) to the EMBL/Genbank/DBJL databases.

DR EMBL: AF177936; AAD55772.1; -

DR HSSP: P03372; IHCP.

DR INTERPRO: IPR000324; -

DR INTERPRO: IPR000324; -

DR INTERPRO: IPR001628; -

DR INTERPRO: IPR001723; -

DR PFAM: PF00104; hormone\_rec; 1.

KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;









01 MAY 2000 (ITERMUTED, 15, last sequence update)  
 02 01 MAY 2000 (ITERMUTED, 15, last annotation update)  
 03 ESTROGEN RECEPTOR BETA (EPVABENT)  
 04 Musca muscula (Rhesus monkey)  
 05 Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:  
 06 Mammalia: Eutheria: Primates: Catarrhini: Cercopithecoidea:  
 07 Cercopithecidae: Macaca  
 08 NBL1taxid: 9544  
 09 [1]  
 10 SEQUENCE FROM N.A.  
 11 MA W X H Smith et al., Nat Biotech 19: 77  
 12 "Polymorphic distribution of Epilypa and Epilypa MENA in intracellular  
 13 tissues of the primate rhesus monkey."  
 14 Am J Physiol 279: 1199-1199 (2000)  
 15 EMBL: AF192249: AAG54069.1  
 16 HSSV: F03472: 1ERE  
 17 INTERPRO: IPR000536:  
 18 INTERPRO: IPR001724:  
 19 INTERPRO: IPR001728:  
 20 PFAM: PF00104: hormone\_recep\_1  
 21 PRINTS: PR00476: STROB-PM-NER  
 22 PRINTS: PR00476: THRE-THRE-8MR  
 23 Reciprocal:  
 24 NBL1taxid: 9544  
 25 NBL1taxid: 9544  
 26 NBL1taxid: 9544  
 27 SEQUENCE 279 AA: 41105 MW: 858097100100301 CRC64:

Query Match 49.4% Score 1998 106 % Length 279  
 Best Local Similarity 96.2% Evid. No. 4 to 114  
 Match 279: Conserved 190 % Mismatch 22 Indels 0 Gaps 0

01 01 MAY 2000 (ITERMUTED, 15, last sequence update)  
 02 01 MAY 2000 (ITERMUTED, 15, last annotation update)  
 03 ESTROGEN RECEPTOR BETA (EPVABENT)  
 04 Musca muscula (Rhesus monkey)  
 05 Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:  
 06 Mammalia: Eutheria: Primates: Catarrhini: Cercopithecoidea:  
 07 Cercopithecidae: Macaca  
 08 NBL1taxid: 9544  
 09 [1]  
 10 SEQUENCE FROM N.A.  
 11 MA W X H Smith et al., Nat Biotech 19: 77  
 12 "Polymorphic distribution of Epilypa and Epilypa MENA in intracellular  
 13 tissues of the primate rhesus monkey."  
 14 Am J Physiol 279: 1199-1199 (2000)  
 15 EMBL: AF192249: AAG54069.1  
 16 HSSV: F03472: 1ERE  
 17 INTERPRO: IPR000536:  
 18 INTERPRO: IPR001724:  
 19 INTERPRO: IPR001728:  
 20 PFAM: PF00104: hormone\_recep\_1  
 21 PRINTS: PR00476: STROB-PM-NER  
 22 PRINTS: PR00476: THRE-THRE-8MR  
 23 Reciprocal:  
 24 NBL1taxid: 9544  
 25 NBL1taxid: 9544  
 26 NBL1taxid: 9544  
 27 SEQUENCE 279 AA: 41105 MW: 858097100100301 CRC64:

01 01 MAY 2000 (ITERMUTED, 15, last sequence update)  
 02 01 MAY 2000 (ITERMUTED, 15, last annotation update)  
 03 ESTROGEN RECEPTOR BETA (EPVABENT)  
 04 Musca muscula (Rhesus monkey)  
 05 Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:  
 06 Mammalia: Eutheria: Primates: Catarrhini: Cercopithecoidea:  
 07 Cercopithecidae: Macaca  
 08 NBL1taxid: 9544  
 09 [1]  
 10 SEQUENCE FROM N.A.  
 11 MA W X H Smith et al., Nat Biotech 19: 77  
 12 "Polymorphic distribution of Epilypa and Epilypa MENA in intracellular  
 13 tissues of the primate rhesus monkey."  
 14 Am J Physiol 279: 1199-1199 (2000)  
 15 EMBL: AF192249: AAG54069.1  
 16 HSSV: F03472: 1ERE  
 17 INTERPRO: IPR000536:  
 18 INTERPRO: IPR001724:  
 19 INTERPRO: IPR001728:  
 20 PFAM: PF00104: hormone\_recep\_1  
 21 PRINTS: PR00476: STROB-PM-NER  
 22 PRINTS: PR00476: THRE-THRE-8MR  
 23 Reciprocal:  
 24 NBL1taxid: 9544  
 25 NBL1taxid: 9544  
 26 NBL1taxid: 9544  
 27 SEQUENCE 279 AA: 41105 MW: 858097100100301 CRC64:

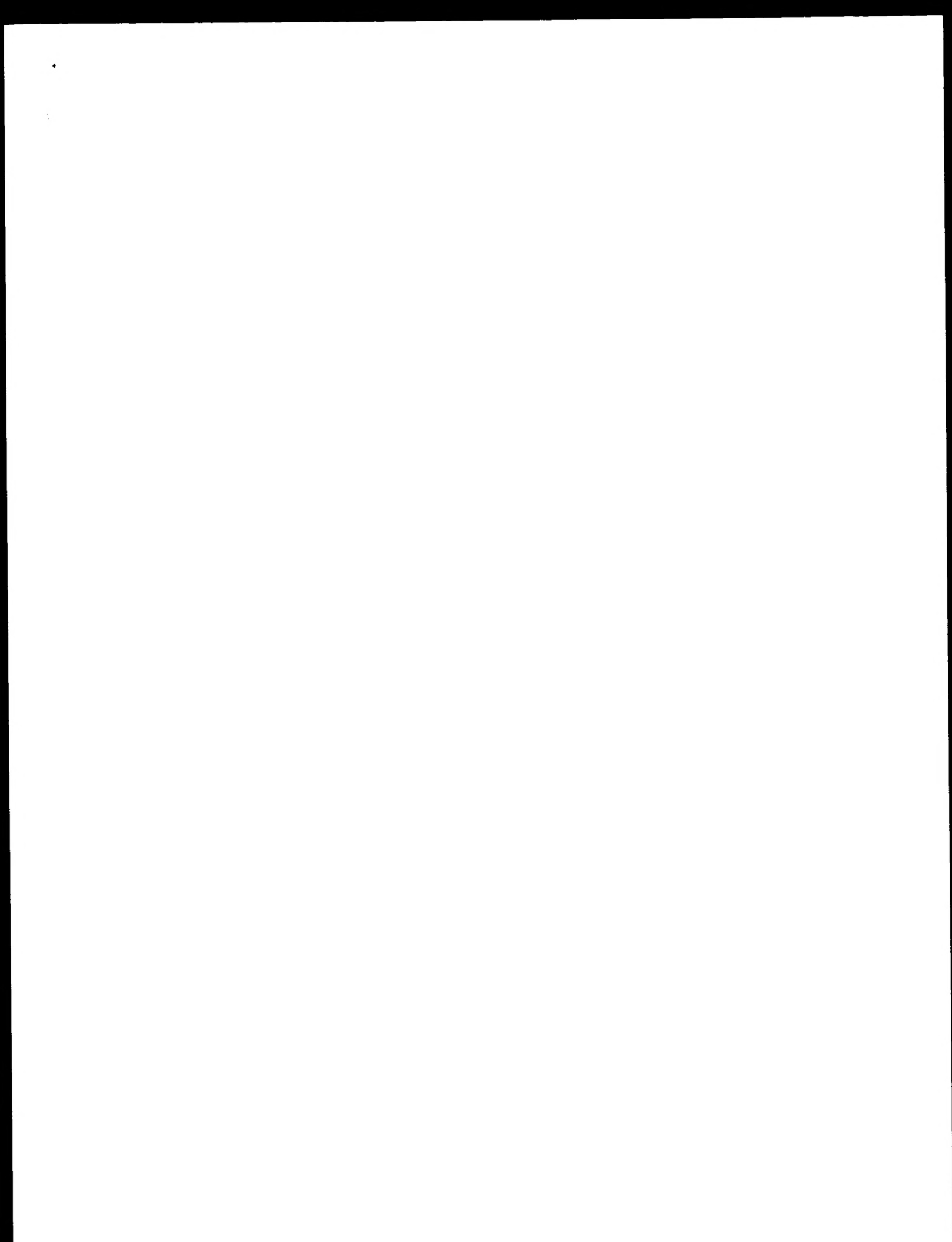
Query Match 49.4% Score 1998 106 % Length 279  
 Best Local Similarity 96.2% Evid. No. 4 to 114  
 Match 279: Conserved 190 % Mismatch 22 Indels 0 Gaps 0

01 01 MAY 2000 (ITERMUTED, 15, last sequence update)  
 02 01 MAY 2000 (ITERMUTED, 15, last annotation update)  
 03 ESTROGEN RECEPTOR BETA (EPVABENT)  
 04 Musca muscula (Rhesus monkey)  
 05 Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:  
 06 Mammalia: Eutheria: Primates: Catarrhini: Cercopithecoidea:  
 07 Cercopithecidae: Macaca  
 08 NBL1taxid: 9544  
 09 [1]  
 10 SEQUENCE FROM N.A.  
 11 MA W X H Smith et al., Nat Biotech 19: 77  
 12 "Polymorphic distribution of Epilypa and Epilypa MENA in intracellular  
 13 tissues of the primate rhesus monkey."  
 14 Am J Physiol 279: 1199-1199 (2000)  
 15 EMBL: AF192249: AAG54069.1  
 16 HSSV: F03472: 1ERE  
 17 INTERPRO: IPR000536:  
 18 INTERPRO: IPR001724:  
 19 INTERPRO: IPR001728:  
 20 PFAM: PF00104: hormone\_recep\_1  
 21 PRINTS: PR00476: STROB-PM-NER  
 22 PRINTS: PR00476: THRE-THRE-8MR  
 23 Reciprocal:  
 24 NBL1taxid: 9544  
 25 NBL1taxid: 9544  
 26 NBL1taxid: 9544  
 27 SEQUENCE 279 AA: 41105 MW: 858097100100301 CRC64:

RN [1]  
 KP SEQUENCE FROM N.A.  
 RC TISSUE=OVARY;  
 RA Xia Z., Gale W.L., Chang X., Langenau D., Patino R., Maule A.G.,  
 RT Penmore L.D.;  
 RT Phylogenetic sequence analysis, recent/ant expression, and tissue  
 RT distribution of a channel catfish estrogen receptor beta.\*  
 RL Blochim, Biophys. Acta 1490:145-152(2000).  
 DK EMBL: AF185368; AAF6157.1; -;  
 KW Receptor.  
 SQ SEQUENCE 575 AA; 64907 MW; E3863C6AB8E824F CRC64;  
 Query Match 49.2%; Score 1381; DB 13; Length 575;  
 Best Local Similarity 53.9%; Pred. No. 34e-112;  
 Matches 297; Conservative 64; Mismatches 112; Indels 78; Gaps 15;  
 QY 13 SPSSVNSQSIILPLEHGSIVPSVDHHPYDAMTPGPAANNYSITSNVNLGCGGRQ 72  
 DB 25 PSNY---PIALGVDRGIVCIPSPYALDGH-----AEMSGGSPADENPAIAP--- 68  
 QY 73 TTFNVNLP--RQH SPLVHQI.SHIYAEQ--KSPWCEARSLHTLPVNRITKR-KV 128  
 DB 69 FLSPSLWSSNHPAMALPLHCPALPYSLPHITAWDRK--PHISGHSFLSPKIL 126  
 QY 129 SCNRCAQVATGNS .....KRGHCAVCSDVYASGYHCVMSGCGCKA 171  
 DB 127 FGRK LLDGDDLEALDDELSSSGAVVKKRDMHCVCVCHDAAGYHGVMSGCGCKA 183  
 QY 172 FFKSVGQNDIA LTA-NKSTIGKRSYACVLEPQ VEVNVPFGSPREPQYPLVKR 231  
 DB 184 FFKSVGQNDY LCPALNGLDNNKRSYVACGLKCTCYMCKGAPREPQYVASRR 243  
 QY 232 -----SGADEQHPFA---GFAKFGSGIAP-KVELLLALSTEDL 268  
 DB 244 TAPMRDASAPVGVKQSGDRLPHPLHVSLSIVSRASASG-----FSGLSPEQL 294  
 QY 269 VLTLLAPPHVILSRP-SAPFTASMMMSITKLAQKELVHMTSMARKIPGEVLSIFDQ 327  
 DB 295 VYCLLAEPQVYLKQCKMPYESTVMMSLTQADKELVLMISMAKIPGEVLSIAHQ 354  
 QY 328 VRLIESQMMVLMQIMWRSIDHGRKILFAPDVLIDRCKCYGKILEITDMLATTSRF 387  
 DB 355 VGLIDCKMCLVLMQIMWRSIDHGRKILFSLDKLNDKNGVGLMEIPDMLACSSRF 414  
 QY 388 RELKIAHKREYLVKAMILNNSMYPLVAPD-DADSSRKLAHLNATDIALVAVIAKSGI 446  
 DB 415 KIKLGNKREYLVKALILNNSMYPLVAPD-DADSSRKLAHLNATDIALVAVIAKSGI 474  
 QY 447 SSQGSQMGCLANLMLSHVHANSKGMEDHLANKCKNVVAVYDILLEMNAHVI--RGCK 504  
 DB 475 STQGSQAKLAHLMLSHVHANSKGMEDHLANKCKNVVAVYDILLEMNAHVSRRHS 534  
 QY 505 SSITGSECSHA 515  
 DB 535 TSVCTPVTIA 545  
 RESULT 14  
 QYH32 PRELIMINARY: PRT: 610 AA.  
 AC QYH32;  
 DT 01-OCT-2000 (TREMURel. 15, Created)  
 DT 01-OCT-2000 (TREMURel. 15, Last sequence update)  
 DE BSIKOBEN RECEPTOR BETA2.  
 OS Carassius auratus (Goldfish).  
 OC Actinopterygii: Neopterygii: Chordata: Vertebrata: Euteleostomi:  
 OC Cypriniformes: Cyprinidae: Cyprinidae: Carassius.  
 OX NCBI\_Taxid=7957;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE=BRAIN/PITUITARY;  
 RA Ma C.H., Dong K.W., Yu K.L.;  
 RT cDNA cloning and expression of a novel estrogen receptor beta-subtype  
 RT in goldfish (Carassius auratus).\*  
 RL Blochim, Biophys. Acta 1490:145-152(2000).  
 DK EMBL: AF177465; AAF35170.1; -;  
 KW Receptor.  
 SQ SEQUENCE 610 AA; 67851 MW; D29FZGDFG165067 CRC64;  
 Query Match 49.1%; Score 1378.5; DB 13; Length 610;  
 Best Local Similarity 51.1%; Pred. No. 6e-112;  
 Matches 304; Conservative 71; Mismatches 141; Indels 89; Gaps 15;  
 QY 6 SPSSLSPPSSVNSQSIILPLEHGS-----ITSSVYVSHDEY-----AM 47  
 DB 13 SPVQANGNSPN-----ILPILYTSGLDMGSGTCTPSPYVAVDQYSPRGGELSGKALT 68  
 QY 48 FYSVA---VMNYSFVSVTILKLSQKQTSF RVMWLP-PQH-----SPLVYHR 93  
 DB 69 LYSFSSPVLAGYTHP-----PVSESLVPSNALSALFMPHPHSPHSLSHSPSLAYKE 119  
 QY 94 QLSHVAFPFESVCEAS-LEHTLVYBELAKKVAQTHFAAGVAGGCKKAAHFAV- 172  
 DB 120 THAHTTWEDAKTHINSSSVYTHA-----KLDGQGLDQDQDQDINSPTQADKQIHFGVAG 174  
 QY 153 SPVAVYHVVVWSPGCTGATTFEELTGNEYVTAFAVLTTLFQKAVFAVAGVAV 212  
 DB 175 HDVASGYHGVMSGCGCKAFAKPKKPSLYGNDYLPVATWGLDQSGSPQGMQELPKGVYV 244  
 QY 213 GMYGSGSRERPGYRVHNSAFAVDFKZAKAPSPGQVAVVCEVLLTA----- 262  
 DB 235 GMYGSGSRERPGYRVHNSAFAVDFKZAKAPSPGQVAVVCEVLLTA----- 262  
 QY 262 ---LSPDQVLTLLAPFPHVILSRP-SAPFTASMMMSITKLAQKELVHMTSMARKIP 314  
 DB 294 AEGCGNLSPDQVLTLLAPFPHVILSRP-SAPFTASMMMSITKLAQKELVHMTSMARKIP 353  
 QY 315 KIRGVYLSLEFDVRLIFSMVIMWRSIDHGRKILFAPDVLIDRCKCYGKILEITDMLATT 474  
 DB 354 KIRGVYLSLEFDVRLIFSMVIMWRSIDHGRKILFAPDVLIDRCKCYGKILEITDMLATT 474  
 QY 375 FIKMGLATTSRRPRKIQGFYVYVKAMILNNSMYPLVAPD-DADSSRKLAHLNATDIALVAV 433  
 DB 414 EIPDMLATTSSRRPRKIQGFYVYVKAMILNNSMYPLVAPD-DADSSRKLAHLNATDIALVAV 473  
 QY 434 TDAVAVYIAKSGISQGSQMGCLANLMLSHVHANSKGMEDHLANKCKNVVAVYDILLEM 493  
 DB 474 TDAVAVYIAKSGISQGSQMGCLANLMLSHVHANSKGMEDHLANKCKNVVAVYDILLEM 533  
 QY 493 MEVAHVIPTGKSTTSFTG .....PALESSEKPSQNGVSGO 530  
 DB 534 MIDANTSQSSBMLAVITKASIPMLTQGTRELLHSKGVAKLSNQPFRSHQAE 588  
 RESULT 15  
 QYH32 PRELIMINARY: PRT: 557 AA.  
 AC QYH32;  
 DT 01-MAY-1999 (TREMURel. 10, Created)  
 DT 01-MAY-1999 (TREMURel. 10, Last sequence update)  
 DE TYPE II ESTROGEN RECEPTOR.  
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
 OC Actinopterygii: Neopterygii: Teleostei: Euteleostomi: Euteleostomi:  
 OC Acanthomorpha: Acanthopterygii: Perciformes: Perciformes: Labroidae:  
 OC Cichlidae: Oreochromis.  
 OX NCBI\_Taxid=8126;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Chang X.T., Kobayashi T., Todo T., Yoshitani Y., Ikoumi T.,  
 RA Kajitani H., Nakamura M., Nishihama Y.;







XX This sequence represents a novel oestrogen binding protein isolated from  
 CC human testis cDNA in order to study upstream translation initiation  
 CC codons using a RACE-PCR technology. This receptor is able to bind and  
 CC be activated by estradiol, estrone and estradiol, can be used in a screening  
 CC assay for the identification of new drugs e.g. novel ligands of hormonal  
 CC analogues.

XX Sequence 530 AA:

Query Match: 100.0%; Score 241; DB 18; Length 530;  
 Best Local Similarity 100.0%; Pred. No. 3e-23;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALKNSPSSINSNSNSGSHLPHGSHYITSSVDSHHYPA 45  
 DB 1 MALKNSPSSINSNSNSGSHLPHGSHYITSSVDSHHYPA 45

RESULT 2

W97858 standard; Protein: 530 AA.

XX W97858:

DI 07-JUN-1999 (first entry)

DE Human oestrogen receptor-beta.

KW oestrogen receptor-beta; HER-beta; human.

OS Homo sapiens.

PN W09907847-A1.

PD 18-FEB-1999.

PF 20-JUL-1998; 98WO-US14944.

PR 05-APR-1997; 97US-0906365.

FA (AMBP) AMERICAN HOME PROD CORP.

PI Bhat RA, Henderson RA, Hsiao C, Karathanasis SK;

DR WPI: 1999-167424/14.

XX N-PSDB: X24364.

PT Human oestrogen receptor-beta coding sequence - useful in the  
 PT production of human oestrogen receptor-beta and identification of  
 PT human oestrogen receptor-beta interactive compounds

PS Claim 17; Page 42-44; 49pp; English.

XX This polypeptide comprises a full-length human oestrogen receptor-beta  
 CC (HER-beta), including 45 previously unknown N terminal amino acid  
 CC residues that are believed to contribute to the transcription  
 CC activation function of the receptor. The amino acid sequence was  
 CC deduced from the nucleotide sequence (see X24364) of an isolated  
 CC cDNA clone. HER-beta is selectively expressed in the thymus,  
 CC spleen, ovary and testes. The invention encompasses HER-beta  
 CC polypeptides and polypeptides, particularly peptides which  
 CC include residues 1-45 of HER-beta. The invention also provides  
 CC expression systems in which transcriptionally active HER-beta or  
 CC fragments can be produced, as well as screening methods for  
 CC identifying HER-beta agonists and antagonists (including  
 CC tissue-specific oestrogens and anti-oestrogens), and HER-beta  
 CC co-activators and inhibitors.

XX Sequence 530 AA:

Query Match: 100.0%; Score 241; DB 20; Length 530;  
 Best Local Similarity 100.0%; Pred. No. 4e-24;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALKNSPSSINSNSNSGSHLPHGSHYITSSVDSHHYPA 45  
 DB 1 MALKNSPSSINSNSNSGSHLPHGSHYITSSVDSHHYPA 45

RESULT 3

Y07270 standard; Protein: 548 AA.

XX Y07270:

DI 06-JUN-1999 (first entry)

DE Human oestrogen receptor.

KW Human; oestrogen receptor; ligand; bone resorption; metabolic disorder;  
 KW cardiovascular disease; cancer; central nervous system; breast; uterine;  
 KW osteoporosis; ovarian; prostatic diabetes; Alzheimer's disease.

OS Homo sapiens.

PN W09912961-A1.

PD 18-MAR-1999.

PF 04-SEP-1998; 98WO-US18577.

PR 29-MAY-1998; 98GB-0096932.

PR 08-SEP-1997; 97US-0058271.

PR 30-SEP-1997; 97US-0060520.

PR 30-OCT-1997; 97GB-0022884.

FA (MERL) MERCK & CO INC.

PI Wilkinson H;

DR WPI: 1999-229222/19.

DE N-PSDB: X34309.

XX Estrogen receptor

PT Claim 1; Fig 1; 32pp; English.

XX This sequence represents a human oestrogen receptor. The receptor can  
 CC be used to identify ligands that bind to human oestrogen receptor. The  
 CC ligands can be used in a method for preventing or treating an oestrogen  
 CC receptor mediated disease or condition, such as abnormal bone resorption,  
 CC a cardiovascular disease, cancer, metabolic disorders or central nervous  
 CC system disorders. The ligand is especially used to treat osteoporosis,  
 CC breast, uterine, ovarian or prostatic cancer, diabetes or Alzheimer's  
 CC disease.

XX Sequence 548 AA:

Query Match: 100.0%; Score 241; DB 20; Length 548;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-23;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALKNSPSSINSNSNSGSHLPHGSHYITSSVDSHHYPA 45  
 DB 1 MALKNSPSSINSNSNSGSHLPHGSHYITSSVDSHHYPA 45

RESULT 4

W98127 standard; Protein: 414 AA.

XX W98127:

[illegible][illegible]

XX Novel murine oestrogen receptor-beta genes and splice variants  
PI useful for treating oestrogen receptor-beta mediated disorders  
XX  
XX  
XX claim 9; Fig 2b; 89pp; English.

CC The present invention describes the murine complete oestrogen receptor  
CC beta (MER beta c) also designated MER beta-3). The present sequence  
CC represents MER beta-2, which is an isoform of MER beta c. The protein  
CC can be used to screen for agents that modulate or block the interaction  
CC between the ER beta c protein and physiological, stilbene or  
CC triphenylethylene (anti)estrogens. The antibody which binds the protein  
CC can be used for subcellular localisation of the ER beta protein and  
CC complementary nucleic acid can be used to inhibit expression of the  
CC ER beta c nucleic acid.

SO Sequence 510 AA;

Query Match 84.2%; Score 203; DB 20; Length 510;  
Best Local Similarity 84.4%; Pred. No. 2,4e-18;  
Matches 38; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 MDKNSPSSLSNPSGSSSTLPLEHSGTYPSSVDSHEEPA 45  
ID 20 meknspslsnpsgssstlplehsgttypssvdsheepa 64

RESULT 7  
W98126  
ID W98126 standard; protein; 510 AA.

AC W98126;  
XX  
XX 21-JUN-1999 (first entry)

DE Mouse oestrogen receptor beta isoform MER beta-2.

KW oestrogen receptor; ER beta-2; ER beta-c; mouse; tumour;  
diagnosis; therapy; isoform.

XX Mus musculus.

XX W09905170-A1.

XX 04-FEB-1999.

XX 28-JUL-1998; 98WO-0515549.

XX 30-JUL-1997; 97US-0054210.

XX 28-JUL-1997; 97US-0053869.

XX (UYVA ) UNIV YALE.

PI Denton R, Fraslon C, Galton R, Rische-Rigon M;  
XX  
XX WPI: 1999-142852/12.

PT Human oestrogen receptor beta-3 - useful in treating and monitoring  
tumours

XX Example 2; Fig 2b; 89pp; English.

CC The present sequence is alternatively spliced isoform MER beta 2  
CC or the murine complete oestrogen receptor-beta (ER beta-c, or  
CC MER beta-3). The MER beta-3 gene (see X24935) contains 9 exons,  
CC including the newly described exon 5B, which is not found in ER  
CC beta-1. Exon 5B is located in the ligand binding domain of MER  
CC beta-3, and probably plays a significant role in MER beta-3 function.  
CC The MER beta-2 clone was isolated from an embryonic stem cell  
CC genomic library. It lacks exon 3. 2 other isoforms, MER beta-1  
CC (see W98125) and rat ER beta-4 (see W98127), have also been

CC isolated, and the human exon 5B region (see X24934) has been  
CC identified. Based on these sequences, the invention provides  
CC methods for identifying agents that block or augment ER beta c  
CC mediated transcriptional regulation, methods to determine whether  
CC ER beta-c or its isoforms is being expressed in tissues or cells,  
CC and methods of identifying and using agents that block the  
CC transcriptional regulation of genes by ER beta c or its isoforms,  
CC which in turn modulates other biological and pathological  
CC processes. Gene therapy expression of ER beta c is envisaged.

SO Sequence 510 AA;

Query Match 84.2%; Score 203; DB 20; Length 510;  
Best Local Similarity 84.4%; Pred. No. 2,4e-18;  
Matches 38; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 MDKNSPSSLSNPSGSSSTLPLEHSGTYPSSVDSHEEPA 45  
ID 20 meknspslsnpsgssstlplehsgttypssvdsheepa 64

RESULT 8  
Y04434  
ID Y04434 standard; protein; 549 AA.

AC Y04434;

XX 25-JUN-1999 (first entry)

DE Murine MER beta-1 clone protein sequence.

KW Estrogen receptor beta; oestrogen receptor beta; ER beta.

XX Mus sp.

XX W09905171-A1.

XX 04-FEB-1999.

XX 28-JUL-1998; 98WO-0515540.

XX 30-JUL-1997; 97US-0054210.

XX 28-JUL-1997; 97US-0053869.

XX (UYVA ) UNIV YALE.

PI Baron R, Chambron P, Denton R, Dupont S, Garnier J;  
XX  
XX WPI: 1999-142853/12.

PT Novel murine oestrogen receptor-beta genes and splice variants -  
useful for treating oestrogen receptor-beta mediated disorders

XX Claim 9; Fig 2a; 89pp; English.

CC The present invention describes the murine complete oestrogen receptor  
CC beta (MER beta c) also designated MER beta-3). The present sequence  
CC represents MER beta-1, which is an isoform of MER beta c. The protein  
CC can be used to screen for agents that modulate or block the interaction  
CC between the ER beta c protein and physiological, stilbene or  
CC triphenylethylene (anti)estrogens. The antibody which binds the protein  
CC can be used for subcellular localisation of the ER beta protein and  
CC complementary nucleic acid can be used to inhibit expression of the  
CC ER beta c nucleic acid.

SO Sequence 549 AA;

Query Match 84.2%; Score 203; DB 20; Length 549;  
Best Local Similarity 84.4%; Pred. No. 2,6e-18;  
Matches 38; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```

07      1 MCKKNSLSNLSNVSYNLSQSLTLEHNSVLYSVSSVSHHEPYA 45
08      LLLLLLLL LL LLLLLLLLLLLLLL LLLLLLLL LLL L
09      ZR MCKKSSSLSPSSYSSLSLLPLEHPHYLPSSYSVSSTHGYSA 64

RESULT          9
WHLZ'
ID      W08125 standard; Protein: 549 AA.
XX
AA      W08125
XX
01      Z1-PDN-1777 (first entry)
XX
XX      Mouse oestrogen receptor beta isoform mck-beta-1.
XX
XX      cDNA clone, receptor: ER beta-1; ER beta-1; mouse; tumour;
XX      diethylstilboestrol-type isoform.
XX
XX      Mus musculus.
XX
XX      W0905170-A1.
XX
XX      03-FEB-1997.
XX
XX      ZR JHL-19967. 96WU-05S15539.
XX
XX      00-JUL-1997? 97US-06F4210.
XX      PR      28-JUL-1997? 97US-06F40694.
XX
XX      (HYPA ) ONLY VALUE.
XX
XX      Location K, Fraction C, Galien K, Kische-Rigon M;
XX
XX      WP1: 1999-142852/12.
XX
XX      Human oestrogen receptor beta-3 - useful in treating and monitoring
XX      tumours.
XX
XX      Example 2: Fig 2a: 69pp: British.
XX
XX      The present sequence is alternatively spliced isoform mck-beta-1
XX      of the murine complete oestrogen receptor beta (ER beta-c), or
XX      mck-beta-1). The mck-beta-1 gene (see X44945) contains 9 exons,
XX      including the newly described exon 5B, which is not found in ER
XX      beta-1. Exon 5B is located in the E and binding domain of mck-
XX      beta-1, and probably plays a significant role in mck-beta-3 function.
XX      The mck-beta-1 clone was isolated by RT-PCR of mRNA, and by
XX      amplification from a mouse embryonic stem cell genomic DNA library.
XX      It lacks exons 5B. Preliminary data indicate that the mck-beta-1
XX      isoform may be more active than the full-length mck-beta-3 (see
XX      W08126). 2 other isoforms, mck-beta-2 (see W08126) and rat ER
XX      beta-3 (see W08127), have also been isolated, and the human exon 5B
XX      portion (see X44944) has been identified. Based on these sequences,
XX      the following five methods for identifying species that show or
XX      absent ER beta-c mediated transcriptional regulation, methods to
XX      determine whether ER beta-c of its isoforms is being expressed in
XX      tissues or cells, and methods of identifying and using agents that
XX      block the transcriptional regulation of genes by ER beta-c or its
XX      isoforms, which in turn modulates other biological and pathological
XX      processes, are hereby disclosed. ER beta-c is envisaged.
XX
XX      Sequence: 143 AA:
XX
XX      Entry March 04-29. Score 2007. Dh 20: Length 549;
XX      first local similarity: 84.4%; Fred. No. 2, Sec 18;
XX      Marches: 02; Character: 02; Miscellaneous: 4, Index: 0, Gaps: 0.


```

[illegible]









DB 585 KLRGSSANSQSGLDPTHTNSVHSNFSYSDHE 619

# RESULT 2

US-08-476-843-5

Sequence 5, Application US/08376843

Patent No. 5846764

GENERAL INFORMATION:

APPLICANT: De-Maggio, Anthony J.

APPLICANT: Hoskstra, Mel F.

TITLE OF INVENTION: Materials and Methods Relating to Proteins

TITLE OF INVENTION: that Interact with Casein Kinase I

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Loole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 231 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/376,843

FILING DATE:

CLASSIFICATION: 445

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/184,605

FILING DATE: 21-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: No. 5846764 and, Greta E.

REGISTRATION NUMBER: 35,302

REGISTERED: 21-JAN-1994

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ. ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 668 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-476-843-5

Query Match 24.38; Score 58.5; DB 2; Length 668;

Best Local Similarity 40.0%; Prod. No. 7.5;

Matches 14; Conservation 5; Mismatches 15; Indels 1; Gaps 1;

QY 9 SANSNSYSNCSSTIP P-HSYLYTSSVINSHE 42

DB 585 NLCSSANSQSGLDPTHTNSVHSNFSYSDHE 619

# RESULT 3

US-07-689-693B-4

Sequence 4, Application US/07689693B

Patent No. 5231011

GENERAL INFORMATION:

APPLICANT: David Hillyard

APPLICANT: Baldemero M. Olivera

TITLE OF INVENTION: Segregated Folding Determinants

TITLE OF INVENTION: for Small Disulfide-Rich Peptides

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Thorpe, No. 5231011th & Western

STREET: 9045 South 700 East, Suite 200

CITY: Sandy

STATE: Utah

COUNTRY: USA

ZIP: 84070

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage

COMPUTER: Compaq LTE/286

OPERATING SYSTEM: DOS 4.01

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/689,693B

FILING DATE: 19910418

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: none

FILING DATE: na

ATTORNEY/AGENT INFORMATION:

NAME: Westerd, M. Wayne

REGISTRATION NUMBER: 22,788

REFERENCE/DOCKET NUMBER: 9925

TELEPHONE: (801) 566-6634

TELEFAX: (801) 566-0750

INFORMATION FOR SEQ. ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: CVIA Omega conotoxin.

IDENTIFICATION METHOD: Direct peptide

IDENTIFICATION METHOD: sequencing of purified Conus geographus

IDENTIFICATION METHOD: venom

US-07-689-693B-4

Query Match 22.8%; Score 55; DB 1; Length 27;

Best Local Similarity 57.98; Prod. No. 0.34;

Matches 11; Conservation 2; Mismatches 6; Indels 0; Gaps 0;

QY 6 SPSSLSNPSNCSSTIP 24

DB 3 SPSSCSPTSNCSNCSNCP 21

# RESULT 4

US-07-689-693B-3

Sequence 3, Application US/07689693B

Patent No. 5231011

GENERAL INFORMATION:

APPLICANT: David Hillyard

APPLICANT: Baldemero M. Olivera

TITLE OF INVENTION: Segregated Folding Determinants

TITLE OF INVENTION: for Small Disulfide-Rich Peptides

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Thorpe, No. 5231011th & Western

STREET: 9045 South 700 East, Suite 200

CITY: Sandy

STATE: Utah

COUNTRY: USA

ZIP: 84070

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage

COMPUTER: Compaq LTE/286

OPERATING SYSTEM: DOS 4.01

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/689,693B

FILING DATE: 19910418

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: none

```

1 FILING DATE: NA
2 ATTORNEY/AGENT INFORMATION:
3 NAME: WOSTER, M. WAYNE
4 REGISTRATION NUMBER: 22,788
5 REFERENCE/KEY NUMBER: 9925
6 TELEPHONE: (601) 566-4443
7 TELEFAX: (601) 566-0750
8 INFORMATION FOR SEQ ID NO: 1:
9 SEQUENCE CHARACTERISTICS:
10 LENGTH: 74 amino acids
11 TYPE: AMINO ACID
12 MODIFIED TYPE: peptide
13 FEATURES:
14 NAME/KEY: prot protide sequence for four-loop
15 NAME/KEY: VIA: Serials Collection from Census geotaphus
16 IDENTIFICATION METHOD: Libraries were created
17 IDENTIFICATION METHOD: using original primed pUC13 vector
18 US-08-624-123-4

```

```

Query Match 22.8% Score 55 DB 1 Length 74
Host Local Similarity 57.9% Prod. No. 1,22
Matches 11: Conservative 2: Mismatches 6: Indels 0: Gaps 0:

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QY 6 SPSSINSTRVNSQSLLP 24
DB 48 SPSSINSTRVNSQSLLP 66

```

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RESULT 5
US-08-624-123-12
1 Sequence 12, Application US/9524124
2 Patent No. 5799276
3 GENERAL INFORMATION:
4 APPLICANT: SHON, KI-JOON
5 APPLICANT: GILLIG, MICHAEL M.
6 APPLICANT: GILVERA, BALDOMERO M.
7 TITLE OF INVENTION: Coccoloxin Peptides
8 NUMBER OF SEQUENCES: 14
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: Wobbe, Bart J et, Howard & Civiletti
11 STREET: 1701 New York Avenue, N.W.
12 CITY: Washington
13 STATE: DC
14 COUNTRY: US
15 ZIP: 20005
16 COMPUTER RELEVABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 SOFTWARE: IBM PC compatible
19 OPERATING SYSTEM: PC DOS/MS DOS
20 CURRENT APPLICATION DATA:
21 FILING DATE: 17-APR-1995
22 TELEPHONE: 202-962-8406
23 TELEFAX: 202-962-8406
24 INFORMATION FOR SEQ ID NO: 1:
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 74 amino acids
27 TYPE: amino acid
28 MODIFIED TYPE: linear
29 FEATURES:
30 NAME/KEY: prot protide
31 NAME/KEY: VIA: Serials Collection from Census geotaphus
32 IDENTIFICATION METHOD: Libraries were created
33 IDENTIFICATION METHOD: using original primed pUC13 vector
34 US-08-624-123-4

```

```

1 TYPE: amino acid
2 STRANDEDNESS: single
3 TOPOLOGY: linear
4 MOLECULE TYPE: protein
5 HYDROPHILIC: No
6 US-08-624-123-12

```

```

Query Match 22.8% Score 55 DB 1 Length 74
Host Local Similarity 57.9% Prod. No. 1,22
Matches 11: Conservative 2: Mismatches 6: Indels 0: Gaps 0:

```

```

QY 6 SPSSINSTRVNSQSLLP 24
DB 48 SPSSINSTRVNSQSLLP 66

```

```

RESULT 6
US-08-624-123-12
1 Sequence 14, Application US/9524124
2 Patent No. 5799276
3 GENERAL INFORMATION:
4 APPLICANT: SHON, KI-JOON
5 APPLICANT: GILLIG, MICHAEL M.
6 APPLICANT: GILVERA, BALDOMERO M.
7 APPLICANT: YOSHIKAWA, JUN
8 APPLICANT: MARSH, KAREN
9 APPLICANT: CHOI, DAVID B.
10 APPLICANT: HILYARD, DAVID R.
11 TITLE OF INVENTION: Coccoloxin Peptides
12 NUMBER OF SEQUENCES: 14
13 CORRESPONDENCE ADDRESS:
14 ADDRESSEE: Wobbe, Bart J et, Howard & Civiletti, LLP
15 STREET: 1701 New York Avenue, N.W., Suite 7000
16 CITY: Washington
17 STATE: DC
18 COUNTRY: U.S.A.
19 ZIP: 20005
20 COMPUTER RELEVABLE FORM:
21 MEDIUM TYPE: Floppy disk
22 SOFTWARE: IBM PC compatible
23 OPERATING SYSTEM: PC DOS/MS DOS
24 CURRENT APPLICATION DATA:
25 FILING DATE: 17-APR-1995
26 TELEPHONE: 202-962-8406
27 TELEFAX: 202-962-8406
28 INFORMATION FOR SEQ ID NO: 1:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 74 amino acids
31 TYPE: amino acid
32 STRANDEDNESS: single
33 TOPOLOGY: linear
34 MOLECULE TYPE: protein
35 HYDROPHILIC: No
36 US-08-624-123-12

```

```

Query Match 22.8% Score 55 DB 1 Length 74
Host Local Similarity 57.9% Prod. No. 1,22
Matches 11: Conservative 2: Mismatches 6: Indels 0: Gaps 0:
QY 6 SPSSINSTRVNSQSLLP 24
DB 48 SPSSINSTRVNSQSLLP 66

```



```

1 APPLICATION NUMBER: US-08/423,944
2 FILING DATE: 06-JUN-1995
3 CLASSIFICATION: 435
4 PRIOR APPLICATION DATA:
5 APPLICATION NUMBER: US-08/440,421
6 FILING DATE: 15-MAY-1995
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: 06/454,516
9 FILING DATE: 21-FEB-1995
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: US-5,405,941
12 FILING DATE: 15-APR-1994
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: 08/423,460
15 FILING DATE: 14-OCT-1994
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: P1/US94/11690
18 FILING DATE: 14-OCT-1994
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: P1/US94/04178
21 FILING DATE: 15-APR-1994
22 ATTORNEY/AGENT INFORMATION:
23 NAME: Giulio A. DeGottis, Jr., Esq.
24 REGISTRATION NUMBER: 41,504
25 REFERENCE/WORK KEY NUMBER: CPT-004DVC12
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: (617) 227-7400
28 TELEFAX: (617) 227-9941
29 INFORMATION FOR SEQ ID NO: 1:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 619 amino acids
32 TYPE: amino acid
33 FEATURE: 1:lipid
34 MULTIPLE TYPE: protein
35 US-08-472,934-12
36
37 Query Match: 22.0%, Score 54, ID 1, Length 619,
38 Host Local Similarity: 46.5%, Prod. No. 47,
39 Matches: 197 Conservative: 57 Mismatches: 18; Indels: 10; Gaps: 3;
40
41 RESULT 1
42 US-08-423,944-4
43 Sequence 4, Application US/08/423,944
44 Patent No. 5,854,043
45 GENERAL INFORMATION:
46 APPLICANT: JOHNSON, GARY L.
47 TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CHL
48 TITLE OF INVENTION: RESPONSIVENESS TO EXTERNAL SIGNALS
49 NUMBER OF SEQUENCES: 10
50 CORRESPONDENCE ADDRESS:
51 ADDRESSEE: SHERIDAN ROSS & MCINTOSH
52 STREET: 1700 LINCOLN STREET, SUITE 4500
53 CITY: DENVER
54 STATE: CO
55 COUNTRY: USA
56 ZIP: 80204
57 COMPUTER READABLE FORM:
58 MEDIUM TYPE: floppy disk
59 OPERATING SYSTEM: IBM PC compatible
60 SOFTWARE: Patco to Release #1.0, Version #1.25
61 CURRENT APPLICATION DATA:
62 REGISTRATION NUMBER: P41,106
63 REFERENCE/WORK KEY NUMBER: CPT-004DVC12
64 TELECOMMUNICATION INFORMATION:
65 TELEPHONE: (617) 227-7400
66 TELEFAX: (617) 227-9941
67 INFORMATION FOR SEQ ID NO: 4:

```

```

1 FILING DATE: 14 APR 1994
2 ATTORNEY/AGENT INFORMATION:
3 NAME: KOVARIK, JOSEPH E.
4 REGISTRATION NUMBER: 43,005
5 REFERENCE/WORK KEY NUMBER: 2679-1-1
6 TELECOMMUNICATION INFORMATION:
7 TELEPHONE: 603/863,9700
8 TELEFAX: 603/863-0234
9 INFORMATION FOR SEQ ID NO: 4:
10 SEQUENCE CHARACTERISTICS:
11 LENGTH: 619 amino acids
12 TYPE: amino acid
13 FEATURE: 1:lipid
14 MULTIPLE TYPE: protein
15 US-08-423,944-4
16
17 Query Match: 22.0%, Score 54, ID 2, Length 619,
18 Host Local Similarity: 46.5%, Prod. No. 47,
19 Matches: 197 Conservative: 57 Mismatches: 18; Indels: 10; Gaps: 3;
20
21 RESULT 1
22 US-08-461,146-4
23 Sequence 4, Application US/08/461,146
24 Patent No. 5,981,205
25 GENERAL INFORMATION:
26 APPLICANT: JOHNSON, GARY L.
27 TITLE OF INVENTION: METHOD FOR REGULATING MEK1 PROTEIN ACTIVITY
28 NUMBER OF SEQUENCES: 14
29 CORRESPONDENCE ADDRESS:
30 ADDRESSEE: Labiva and Vogelhold
31 STREET: 69 State Street
32 CITY: Boston
33 STATE: Massachusetts
34 COUNTRY: U.S.A.
35 ZIP: 02109
36 COMPUTER READABLE FORM:
37 MEDIUM TYPE: floppy disk
38 OPERATING SYSTEM: IBM PC compatible
39 SOFTWARE: Patco to Release #1.0, Version #1.25
40 CURRENT APPLICATION DATA:
41 REGISTRATION NUMBER: P41,106
42 REFERENCE/WORK KEY NUMBER: CPT-004DVC12
43 TELECOMMUNICATION INFORMATION:
44 TELEPHONE: (617) 227-7400
45 TELEFAX: (617) 227-9941
46 INFORMATION FOR SEQ ID NO: 4:

```

SEQUENCE CHARACTERISTICS:  
 LENGTH: 619 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-461-146C-4

Query Match 22.0%; Score 53; DB 2, Length 619,  
 Best Local Similarity 36.5%; Pred. No. 37;  
 Matches 19; Conservative 5, Mismatches 18, Indels 10, Gaps 3;  
 QY 1 MDIKNSPSSLSNP---SSYNGSOSILPLEHGSITYPS-----SYVDSHHEV 43  
 DB 197 MDQMIDPLSLSSPENSNGSGSPSLISPLD-GESEYKSKMPACGYPDNHGEF 247

RESULT 12  
 US-08-461-146C-12  
 Sequence 12, Application US/08461146C  
 Patent No. 5981265  
 GENERAL INFORMATION:  
 APPLICANT: JOHNSON, GARY L.  
 TITLE OF INVENTION: METHODS FOR REGULATING MEKK PROTEIN ACTIVITY  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Lathive and Cockfield  
 STREET: 60 State Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: U.S.A.  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/461,146C  
 FILING DATE: 05-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/354,516  
 FILING DATE: 21-FEB-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/049,754  
 FILING DATE: 15-APR-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/723,460  
 FILING DATE: 14-OCT-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US94/11690  
 FILING DATE: 14-OCT-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US94/04178  
 FILING DATE: 15-APR-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KARA, Catherine J.  
 REGISTRATION NUMBER: P41,106  
 REFERENCE/DOCKET NUMBER: CPT-004CNI  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 227-7400  
 TELEFAX: (617) 227-5941  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 619 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-461-146C-12

Query Match 22.0%; Score 53; DB 2, Length 619;

Best Local Similarity 36.5%; Pred. No. 37;  
 Matches 19; Conservative 5; Mismatches 18; Indels 10; Gaps 3;

QY 1 MDIKNSPSSLSNP---SSYNGSOSILPLEHGSITYPS-----SYVDSHHEV 43  
 DB 197 MDQMIDPLSLSSPENSNGSGSPSLISPLD-GESEYKSKMPACGYPDNHGEF 247

RESULT 13  
 US-08-461-145C-4  
 Sequence 4, Application US/08461145C  
 Patent No. 6074861  
 GENERAL INFORMATION:  
 APPLICANT: JOHNSON, GARY L.  
 TITLE OF INVENTION: NOVEL MEKK PROTEINS  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Lathive and Cockfield, LLP  
 STREET: 60 State Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: U.S.A.  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/461,145C  
 FILING DATE: 5-JUNE-1995  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/049,254  
 FILING DATE: 11-APR-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/723,460  
 FILING DATE: 14-OCT-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US94/11690  
 FILING DATE: 14-OCT-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US94/04178  
 FILING DATE: 15-APR-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/354,516  
 FILING DATE: 21-FEB-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kara, Catherine J.  
 REGISTRATION NUMBER: P-41,106  
 REFERENCE/DOCKET NUMBER: CPT-004CNI  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 227-7400  
 TELEFAX: (617) 227-5941  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 619 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-461-145C-4

Query Match 22.0%; Score 53; DB 4, Length 619;  
 Best Local Similarity 36.5%; Pred. No. 37;  
 Matches 19; Conservative 5; Mismatches 18; Indels 10; Gaps 3;

QY 1 MDIKNSPSSLSNP---SSYNGSOSILPLEHGSITYPS-----SYVDSHHEV 43  
 DB 197 MDQMIDPLSLSSPENSNGSGSPSLISPLD-GESEYKSKMPACGYPDNHGEF 247

RESULT 14



Fri Apr 20 09:00:56 2001

us-08-906-365-2\_copy\_1\_45.ra1

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Kimball, V.M.; Peterson, M.J.; Lee, A.M.; Kemp, D.J.

Mol. Biochem. Parasitol. 57: 261-269, 1993

Abstract: Structure of the apical membrane antigen 1 (AMA-1) of Plasmodium chabaudi.

Accession number: A44964

Accession: A44964

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Accession: A44964

Query Match 23.4% Score 57.146 21 Length 550

Best Local Similarity 49.1% Prod. No. 24

Matches 10 Conserved 10 Mismatches 10

Accession: A44964

Accession: A44964

Accession: A44964

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Accession: A44964

Accession: A44964

Accession: A44964

C:Species: Homo sapiens (man)  
 C:Date: 21-Jul-1995 #sequence\_revision 28 Jul-1995 #text\_change 26-May-2000  
 C:Accession: G56695  
 P:STANDARD: Human homology, C.M.: Redhead, N.J.; Hill, R.E.; Ariavantis-Tsakonas, S.  
 Nature Genet. 2: 119-127, 1992  
 A:Title: Human homologs of a trophoblast enhancer of split gene product define a novel fa  
 A:Reference number: A56695; M010:94265185  
 A:Accession: G56695  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-743 <STL>  
 A:Cross-references: GH:M9436; NID:9307511; P10N:AAA61193.1; F1D:9307512  
 C:Keywords:  
 A:Gene: DB:HLK2; ESC2  
 A:Cross-reference: GDB:228049; OMIM:601041  
 A:Map position: 19p13.3-19p13.3  
 C:Importance: unassigned WD repeat proteins; WD repeat homology  
 C:Keywords: nucleus  
 P:499-532/Domain WD repeat homology <MD>  
 P:585-616/Domain WD repeat homology <MD>  
 P:667-700/Domain WD repeat homology <MD>  
 P:708-741/Domain WD repeat homology <MD>

Query Match 23.2% Score 56; DB 2; Length 743;  
 Best Local Similarity 37.1%; Pred. No. 42;  
 Matches 13; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

OY 6 SSSSLSPSSSYN--SGSTLPIPHGNTVPSVYVSH 40  
 DB 341 SPLTSSPTTSPSSSHSTINDLSVSSVSLH 375

## RESULT 13

membrane atpase - fission yeast (Schizosaccharomyces pombe)  
 C:Species: Schizosaccharomyces pombe  
 C:Date: 02-Nov-1999 #sequence\_revision 0-1-Nov-1999 #text\_change 03-Dec-1999  
 C:Accession: U41055  
 R:Hitler, H.; Inestradotto, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.  
 submitted to the EMBL data library, August 1998  
 A:Reference number: Z21967  
 A:Accession: U41055  
 A:Status: preliminary; Translated from CH/EMBL/MDM1  
 A:Molecule type: DNA  
 A:Residues: 1-1315 <HL>  
 A:Cross-references: EMBL:U40132; F10N:CAA0413.1; GSTR:G000008; SRRB:SP01672.11c  
 A:Experimental source: strain 972b; cosmid c1672  
 C:Keywords:  
 A:Gene: SRRB:SP01672.11c  
 A:Map position: 3

Query Match 23.2% Score 56; DB 2; Length 1315;  
 Best Local Similarity 34.0%; Pred. No. 81;  
 Matches 16; Conservative 6; Mismatches 17; Indels 8; Gaps 1;

OY 4 KNSPSSLSPSSSYN--SGSTLPIPHGNTVPSVYVSH 42  
 DB 10 KRSTSSASKNSLNSYLASSLMSHSDIFDGLGTSIPSSVSSFFHHQ 56

## RESULT 14

S73697  
 Probable X-pro dipeptidase (EC 3.4.13.9) pepX - Mycoplasma pneumoniae (strain A10C 23342  
 N:Alternative names: hypothetical protein P01\_01354  
 C:Species: Mycoplasma pneumoniae  
 A:Variety: A10C 23342  
 C:Date: 18-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
 C:Accession: S73697  
 P:Hitler, H.; Hilbert, H.; Plagens, H.; Pirtl, E.; Li, B.C.; Hettmann, R.  
 Nucleic Acids Res. 24: 4429-4449, 1996  
 A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae

A:Reference number: S73327; M010:97105885

A:Accession: S73697  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-354 <MD>  
 A:Cross-references: EMBL:AB00035; GH:006683; K10:G17014; P10N:AAA66019.1; F1D:94167  
 A:Note: The nucleotide sequence was submitted to the EMBL data library, November 1996  
 C:Keywords: dipeptide hydrolase  
 A:Gene: pepX  
 A:Gene code: SGC3  
 A:Superfamily: X-Pro aminopeptidase

Query Match 23.0% Score 55.5; DB 1; Length 354;  
 Best Local Similarity 40.5%; Pred. No. 21;  
 Matches 15; Conservative 6; Mismatches 9; Indels 7; Gaps 3;

OY 1 MDRKSSSLSPSSSYN--SGSTLPIPHGNTVPSV 34  
 DB 294 LDHHP--NVSISYNKLCHMAVILHES 326

## RESULT 15

NRKNGC  
 omega-conotoxin GVIB precursor [validated] - cone shell (Conus geographus)  
 N:Alternative names: shaker peptide GVIB  
 N:Comments: omega-conotoxin GVIA, omega-conotoxin GVIC  
 C:Species: Conus geographus (geography cone)  
 C:Date: 25-Feb-1985 #sequence\_revision 25-Mar-1995 #text\_change 15-Sep-2000  
 C:Accession: A44006; A60133; B60134; A01785  
 R:Collidge, C.J.; Hunsperger, J.P.; Imperial, J.S.; Hilliard, D.R.  
 Toxicon 30: 1111-1116, 1992  
 A:Title: Precursor structure of omega-conotoxin GVIA determined from a cDNA clone.  
 A:Reference number: A44006; M010:93064266  
 A:Accession: A44006  
 A:Molecule type: mRNA  
 A:Residues: 1-73 <COL>  
 A:Cross-references: GH:M4042; K10:J15625; F10N:AAA1593.1; F1D:91070493  
 A:Experimental source: venom duct

A:Note: Sequence extracted from NCBI backbone (NCBI:U19531, NCBI:U19532)  
 R:Olivera, B.M.; Gray, W.R.; Zeikus, R.; McIntosh, J.M.; Varag, J.; Pivrot, J.; de Sa  
 Science 230: 1348-1343, 1985  
 A:Title: Peptide neurotoxins from fish-hunting cone snails.  
 A:Reference number: A43620; M010:8676213  
 A:Accession: A60133  
 A:Molecule type: protein  
 A:Residues: 46-73 <COL>  
 A:Accession: B60134  
 A:Molecule type: protein  
 A:Residues: 46-71 <COL>  
 R:Olivera, B.M.; McIntosh, J.M.; Cruz, L.; Lague, F.A.; Gray, W.R.  
 Biochemistry 23: 5087-5090, 1984  
 A:Title: Purification and sequence of a presynaptic peptide toxin from Conus geographus  
 A:Reference number: A01785; M010:85072796

A:Accession: A01785  
 A:Molecule type: protein  
 A:Residues: 46-72 <COL>  
 R:Nishiyuchi, Y.; Kuniyoshi, K.; Noda, Y.; Watanabe, T.X.; Sakakibara, S.  
 Biopolymers 25: 561-568, 1986  
 A:Title: Synthesis and secondary-structure determination of omega-conotoxin GVIA: a 2  
 A:Reference number: A49017; M010:87049928

A:Contents: annotation  
 A:Note: disulfide bonds determined and confirmed by chemical synthesis  
 R:Davis, J.H.; Bradley, F.K.; Miljanich, G.P.; Nadasdi, L.; Ramachandran, J.; Basus,  
 submitted to the Brookhaven Protein Data Bank, April 1993  
 A:Reference number: A51894; PDB:1OMC  
 A:Contents: annotation, conformation by (1H NMR, residues 46-72  
 Biochemistry 32: 7356-7405, 1993  
 R:Davis, J.H.; Bradley, F.K.; Miljanich, G.P.; Nadasdi, L.; Ramachandran, J.; Basus,  
 A:Title: Solution structure of omega-conotoxin GVIA using 2-D NMR spectroscopy and re  
 A:Reference number: A58326; M010:9332945  
 A:Contents: annotation; conformation by (1H NMR

Kelland, P.K.; Inagaki, K.M.; Pennington, M.W.; Norton, R.S.  
Submitted to the Brookhaven Protein Data Bank, August 1993

Accession number: A51089; PDB: 100

Abstract: Structural conformation by (1)H-NMR, residues 46-72

Comment: There are several types of conotoxins: alpha, acting on postsynaptic membrane

neurotoxic.

Keywords: omega-conotoxin  
Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel inh

Full 22/2000: Status: predicted - SIG.

Full 22/2000: Status: predicted - PRO.

Full 22/2000: Status: predicted - MATS

Full 22/2000: Status: predicted - MATS

Full 22/2000: Status: predicted - MATS

Full 22/2000: Status: predicted - MATS

Full 22/2000: Status: predicted - MATS

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Full 22/2000: Status: predicted - MATS

Full 22/2000: Status: predicted - MATS

Full 22/2000: Status: predicted - MATS

Search completed: April 19, 2001, 00:34:04  
Job time: 549 sec

1  
2  
3



OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID:9606;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RC TISSUE:OVARY;  
 KA En H., Leygue E., Dodelas H., Watson P.H., Murphy L.C.;  
 KT Cloning and functional characteristics of human estrogen receptor  
 beta isoforms.  
 RT Submitted (JAN 1993) to the EMBL/GenBank/DBJ databases.  
 PI EMBL: AF124790; AAD32580.1;  
 DR HSSP: P03372; 1HCP.  
 DR INTERPRO: IPR000324;  
 DR INTERPRO: IPR001628;  
 DR PFAM: PF00105; 21-c4; 1.  
 DR PRINTS: PR00647; STROD1628.  
 DR PROSITE: PS00031; NUCLEAR\_RECEPTOR\_1.  
 KW Receptor.  
 SQ SEQUENCE 323 AA: 35944 MW: 15837605630A12 CRC64;

Query Match 100.0%; Score 241; DB 4; Length 323;  
 Best Local Similarity 100.0%; Pred. No. 1c-23;  
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 MIKRNPSLSPSSSYNCOSLPLEHGSYIPSSYVDSHNEYA 45  
 DB 1 MIKRNPSLSPSSSYNCOSLPLEHGSYIPSSYVDSHNEYA 45

RESULT 3  
 Q95171 PRELIMINARY; PRT; 530 AA.  
 AC Q95171;  
 DT 01-FEB-1997 (TREMBLER, 02, Created)  
 DT 01-MAY-2000 (TREMBLER, 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBLER, 15, Last annotation update)  
 DE ESTROGEN RECEPTOR BETA.  
 OS Callitrix jacchus (Common marmoset).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callitrix.  
 OX NCBI\_TaxID:9483;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-TESTIS;  
 KA Gaughan J.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 RN 12  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-TESTIS;  
 KA Scoble G.;  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 CC -> SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL: Y09472; CAAT0546.2;  
 DR HSSP: P03372; 1HCP.  
 DR INTERPRO: IPR000324;  
 DR INTERPRO: IFC00536;  
 DR INTERPRO: IPR001628;  
 DR INTERPRO: IPR001723;  
 DR PFAM: PF00104; hormone\_rec\_1.  
 DR PFAM: PF00105; 21-c4; 1.  
 DR PRINTS: PR00047; STROD1628.  
 DR PRINTS: PR00350; VITAMINR.  
 DR PROSITE: PS00031; NUCLEAR\_RECEPTOR\_1.  
 KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;  
 KW Zinc-finger.  
 SQ SEQUENCE 530 AA: 59087 MW: 45089107A44C53D1 CRC64;

Query Match 90.0%; Score 217; DB 6; Length 530;  
 Best Local Similarity 91.1%; Pred. No. 2.4e-20;  
 Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Matches 41; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 OY 1 MIKRNPSLSPSSSYNCOSLPLEHGSYIPSSYVDSHNEYA 45  
 DB 1 MIKRNPSLSPSSSYNCOSLPLEHGSYIPSSYVDSHNEYA 45

RESULT 4  
 Q9JMG7 PRELIMINARY; PRT; 139 AA.  
 AC Q9JMG7;  
 DT 01-OCT-2000 (TREMBLER, 15, Created)  
 DT 01-OCT-2000 (TREMBLER, 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBLER, 15, Last annotation update)  
 DE ESTROGEN RECEPTOR BETA (FRAGMENT).  
 CN ERB.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/c;  
 KA Ishibashi O., Kawashima H.;  
 KT "Cloning and characterization of the promoter region of mouse estrogen  
 receptor beta."  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB044957; BAA92313.1;  
 KW Receptor.  
 SQ SEQUENCE 139 AA: 15215 MW: 4703615A8E994DAB CRC64;

Query Match 84.2%; Score 203; DB 11; Length 139;  
 Best Local Similarity 84.4%; Pred. No. 3.9e-19;  
 Matches 39; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 OY 1 MIKRNPSLSPSSSYNCOSLPLEHGSYIPSSYVDSHNEYA 45  
 DB 20 MIKRNPSLSPSSSYNCOSLPLEHGSYIPSSYVDSHNEYA 64

RESULT 5  
 Q9XSW2 PRELIMINARY; PRT; 163 AA.  
 AC Q9XSW2;  
 DT 01-NOV-1999 (TREMBLER, 12, Created)  
 DT 01-NOV-1999 (TREMBLER, 12, Last sequence update)  
 DT 01-OCT-2000 (TREMBLER, 15, Last annotation update)  
 DE ESTROGEN RECEPTOR BETA (FRAGMENT).  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae Sus.  
 OX NCBI\_TaxID=9623;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 KA Kowalski A.A., Grady L.S., Stancu E.C.M.;  
 RL "Expression of estrogen receptor beta by the porcine embryo during the  
 preimplantation period and its possible role in the regulation of  
 growth."  
 RT growth.  
 RT growth.  
 PI Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF164957; AAD45381.1;  
 DR HSSP: P03372; 1HCP.  
 DR INTERPRO: IPR001628;  
 DR PFAM: PF00105; 21-c4; 1.  
 KW Receptor.  
 KW NON\_TIR.  
 SQ SEQUENCE 163 AA: 17704 MW: FEP9641A3B63181E CRC64;

Query Match 80.1%; Score 193; DB 6; Length 163;  
 Best Local Similarity 82.2%; Pred. No. 9.4e-18;  
 Matches 37; Conservative 3; Mismatches 5; Indels 0; Gaps 0;



01-012  
ID 01-012 PRELIMINARY: 573 AA  
AC 01-012  
DT 01-JUL-1997 (TREMblrel. 04, created)  
D1 01-JUL-1997 (TREMblrel. 04, last sequence update)  
D2 01-OCT-2000 (TREMblrel. 15, last annotation update)  
DE ESTROGEN RECEPTOR.  
OS Anguilla japonica (Japanese eel).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;  
OC Anguilla japonica.  
OX NCBI\_TaxID:7947;  
PN 11  
RP SEQUENCE FROM N.A.  
RC TISSUE: LIVER;  
RA Tissue Loc.:  
RT Submitted (Apr-1997) to the EMBL/Genbank/DBP databases.  
KN 12  
KP SEQUENCE FROM N.A.  
RC TISSUE: LIVER;  
RA Tissue Loc.:  
RT Molecular cloning and characterization of Japanese eel estrogen  
receptor cDNA.  
RL Mol. Cell. Endocrinol. 119:37-45(1996).  
CC 1- SURCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
EMBL: AB003356; HAI19651.1;  
DR HSSP: P03372; ITC;  
DR INTERPRO: IPR000546;  
DR INTERPRO: IPR001628;  
DR INTERPRO: IPR001723;  
DR PFAM: PF00104; hormone\_rec\_1.  
DR PFAM: PF00105; zf-C4\_1.  
DR PRINTS: PR00047; STROUDINGER.  
DR PRINTS: PR00198; STROUDINGER.  
DR PRINTS: PR00198; STROUDINGER.  
DR PRE-SITE: PS00031; NUCLEAR\_RECEPTOR; 1  
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;  
KW Zinc-finger.  
SO SEQUENCE 573 AA; 63420 MW; 9C6AC1D8D39ED4CC CRC64;

Query Match 40 74: Score 73. DB 13: Length 573;  
Best Local Similarity 42.48; Pred. No. 0.17;  
Matches 14: Conservative 6; Mismatches 13; Indels 0; Gaps 0;

01-012  
ID 01-012 PRELIMINARY: 573 AA  
AC 01-012  
DT 01-JUL-1997 (TREMblrel. 04, created)  
D1 01-JUL-1997 (TREMblrel. 04, last sequence update)  
D2 01-OCT-2000 (TREMblrel. 15, last annotation update)  
DE ESTROGEN RECEPTOR.  
OS Anguilla japonica (Japanese eel).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;  
OC Anguilla japonica.  
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PN 11  
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KN 12  
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RT Molecular cloning and characterization of Japanese eel estrogen  
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RL Mol. Cell. Endocrinol. 119:37-45(1996).  
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D2 01-OCT-2000 (TREMblrel. 15, last annotation update)  
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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KW Zinc-finger.  
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Fri Apr 20 09:01:00 2001

us-08-906-365-2\_copy\_1\_45.rspt

Page 6

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Job time: 14736 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

08 protein : protein search, using sw model.

Run on: April 19, 2001, 10:45:31 : Search time 51.46 Seconds

(without alignments)

29,955 Million cell updates/sec

1 hit per  
protein score: 241

Sequence: 1 MURKSPSSINRPSSTVNR.....EHSIVPSYVSHHEVYA 45

Scoring table:  
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Gapop: 10.0 , Gapext: 0.5

Searched: 9445 seqs, 4425486 residues

Total number of hits satisfying chosen parameters: 9445

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post processing: Minimum Match: 0%

Listing first 45 summaries

Database: 1 SWISSPROT\_1994\*

Prod. Scores are the number of residues predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	Description
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2	217	90.0	540	1	ESR2_VALLA
3	205	85.1	540	1	ESR2_RAT
4	203	84.2	540	1	ESR2_MOUSE
5	193	80.1	164	1	ESR2_PIG
6	193	80.1	527	1	ESR2_BOVIN
7	193	80.1	527	1	ESR2_SHEEP
8	141	58.5	524	1	ESR2_STOVU
9	73	25.3	573	1	ESR2_ANCIA
10	61.5	25.5	508	1	ESR1_CARAU
11	58.5	24.3	664	1	YER1_YEAST
12	57	23.7	598	1	AMAL_PLANT
13	56.5	23.4	612	1	YRBB_YEAST
14	56	23.4	273	1	YFBA_YAC11
15	56	23.2	445	1	HLSX_HUMAN
16	56	23.2	743	1	HLFX_HUMAN
17	56	23.2	1315	1	ALC9_SCHUO
18	55.5	23.0	354	1	AMPD_MYCIN
19	55.5	23.0	673	1	ESR2_MITCN
20	55	22.8	73	1	OX06_MOUSE
21	55	22.8	243	1	G112_RAT
22	55	22.8	766	1	EYA2_HUMAN
23	55	22.8	909	1	ANL2_HUMAN
24	54.5	22.5	335	1	D4H1_RAT
25	54.5	22.5	868	1	SRRC_DROME
26	54	22.1	213	1	Y112_MOUSE
27	54	22.1	398	1	YAXL_RHUS
28	53.5	22.2	612	1	YND4_YEAST
29	53.5	22.2	1146	1	YHC3_YEAST
30	53	22.0	619	1	M4K2_MOUSE
31	53	22.0	1182	1	ETRE_HUMAN
32	52.5	21.8	449	1	M053_NYCA
33	52.5	21.8	1176	1	C1AA_BACIK

34	52.5	21.8	1176	1	C1AA_BACIK
35	52.5	21.8	1176	1	C1AA_BACIK
36	52	21.6	107	1	FER_PSAIA
37	52	21.6	559	1	E312_SALAE
38	52	21.6	636	1	YND6_YEAST
39	52	21.6	647	1	YK1_YEAST
40	52	21.6	1014	1	MDL1_HUMAN
41	52	21.6	1189	1	C10A_BACT
42	51.5	21.4	346	1	C101_HUMAN
43	51.5	21.4	349	1	Y028_P90
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#### ALIGNMENTS

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DI 15-JUL-1994 (Ref. 38, last sequence update)  
DT 01-OCT-2000 (Ref. 45, last annotation update)  
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OX NCBI\_Taxid 9606;  
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RX MEDLINE=98134678; PubMed=947341;  
RA Okawa S., Inoue S., Watanabe T., Hiroi H., Ogino A., Hasegawa T., Onodera Y., Muramatsu M.;  
RT "The complete primary structure of human estrogen receptor beta (ER-beta) and its heterodimerization with ER-alpha in vivo and in vitro."  
RI Biochem. Biophys. Res. Commun. 241:122-127 (1998).  
RI [2]  
RN SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.  
RP TISSUE-TOSTIS: and breast;  
RX MEDLINE=98104246; PubMed=94667;  
RA Moore J.T., Moyer D.D., Shetty K., Maiti T., Lee S.A., Horne E.L., Su J.-L., Kliber S.A., Lehmann D.M., Winters J.M.;  
RT "Cloning and characterization of human estrogen receptor beta isoforms."  
RI Biochem. Biophys. Res. Commun. 247:75-79 (1998).  
RN [3]  
RP SEQUENCE OF 46 529 FROM N.A. (USP-8M BETA 1), AND CHARACTERIZATION OF TISSUE-TOSTIS.  
RX MEDLINE=96454675; PubMed=87961;  
RA Mosselman S., Polman J., Dijkema R.;  
RT "ER beta: identification and characterization of a novel human estrogen receptor."  
RI FEBS Lett. 402:49-53 (1996).  
RN [4]  
RP SEQUENCE FROM N.A. (USP-8M BETA 2), AND CHARACTERIZATION OF TISSUE-TOSTIS.  
RX MEDLINE=98437908; PubMed=967411;  
RA Okawa S., Inoue S., Watanabe T., Ogino A., Hiroi H., Onodera Y., Muramatsu M.;  
RT "Molecular cloning and characterization of human estrogen receptor beta (a potential inhibitor of estrogen action in human)."  
RI Nucleic Acids Res. 27:5705-5712 (1999).  
RN [5]  
RP SEQUENCE OF 54 530 FROM N.A. (USP-8M BETA 1A AND BETA 1.2).  
RX TISSUE-Endometrium;  
RA Brandenberger A.W., Lefebvre D., Lignon R.N., Lefebvre P.M.;  
RT "Subcloning and sequencing of the ER-beta gene from human endometrium."  
RI [6]  
RN SEQUENCE FROM N.A. (USP-8M BETA 2A).  
RP

















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RL      Curr. Microbiol. 37:356-358(1998).
CC      -1- FUNCTION: THIS ENTRY IS CONSIDERED AS A BIFUNCTIONAL ENZYME,
CC      POSSESSING TWO ACTIVE SITES, ONE AN ALCOHOL DEHYDROGENASE AND
CC      THE OTHER AN ALDEHYDE DEHYDROGENASE (BY SIMILARITY)
CC      -1- CATALYTIC ACTIVITY: L-HISTIDINOL + 2 NAD(+) -> L-HISTIDINE +
CC      2 NADH.
CC      -1- PATHWAY: TENTH STEP IN HISTIDINE BIOSYNTHETIC PATHWAY.
CC      -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC      -1- SIMILARITY: TO OTHER PROKARYOTIC, FUNGAL AND PLANTS HDH.
CC
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL Outstation at
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC
CC      EMBL: AF067228; AAC97355.1; -.
CC      InterPro: IPR001692; -.
CC      InterPro: IPR001917; -.
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